79	158	5 229	25 289	45 349	65 409	85 469	105 529	125 589
CGTC	GTGA	۲ħ	G GGT	L CTA	D GAC	FIC	F	GGC
36600	CGGCAAGGGCCATCCGGTGCCACCCATGTCGCACTAGAGCAGAAGAGGGGTGA	V 3 GTG	EGAG	L CTG	A GCG	L	V GTC	L
3TAG(AGAA(L G TTG	S TCC	D GAC	T ACT	CCC	GGC	A GCG
3AGA(3AGC	C TGG	D GAC	A GCC	A GCT	A GCG	R CGC	R CGG
ACCG(ACTA(ACC	P	A GCT	A GCC	$\frac{L}{TTG}$	GGT	Γ
3GGA	rcgc/	M GCTCTGTACTGTCCCTGGTGGTCGCCGCC ATG	T ACC	C TGC	PCCT	W TGG	L	T ACG
ACCT	CATG	CCGC	GGC	I ATC	L TTA	G GGC	A GCG	N AAC
CACA	CACC	3TCG(L TTA	C	E GAG	CCC	D GAT	S TCT
3CCT(GTGC(GGTG(G GGG	K AAA	A GCC	R CGC	L CTA	S TCA
CACC	ICCG	CCCT	V GTT	Y TAC	P CCA	CIG	E GAA	L CTA
3 3 3 3 3	GCCA	\mathtt{CTGT}_0	C G C	P CCC	V GTG	CG R	N AAC	D GAT
3AGT(AAGG	rgra(L	C TGC	D GAC	Q CAG	H CAC	CIC
CTAA(CCCC	CTC	M ATG	N AAC	Q CAG	CIC	D GAC	Γ
3CGG(rccr(AGCT(C TGC	H CAC	CIG	A GCG	L CTA	R AGG
GAGC	IGCC	ACAG	CIC	CIC	999	N AAC	H CAC	L CTG
GGGG	9009	CIEC	CIG	A GCG	L CTA	H CAC	L	G GGC
CGTC	ACCC	CAAC	TACA	R CGT	G GGC	S AGC	A GCC	S AGC
CACG	AAGA	ACTG(GGG	CCC	T ACT	L CIG	R CGC	A GCC
GTCGACCCACGCGTCCGGGGGGGCGCGCGTAAGAGTGCCGCACCGCCTCACAACCTGGGAACCGGAGAGTAGGGGCCGTC	GGCTGGCAAGAACCCGCCGTGCCTCCT	GTCCTGAACTGCAACCTGCACAGAGCT	Γ	P CCG	C TGC	D GAC	L CTG	N AAC
GTC	355	GTC	L	H HHC	S AGC	CHC	Q CAG	V GTC

Fig. 1A

145 649	165 709	185 769	205 829	225 889	245 949	265	285
L TTG	295 66C	L	A GCG	C TGC	FTTT	Q CAG 1	E GAA 1
CG R	L CTG	H CAC	A GCC	D GAC	D GAC	F TTC	P CCG
N AAC	YTAC	T ACC	L CTG	C H	CGC	F TTC	R CGG
N AAT	CIC	A GCC	E GAG	CCT	V GTG	CGC	K AAG
H.H. H.H.C	H CAT	S AGC	P CCT	Γ	A GCC	V GTG	L CTA
L CTG	S AGC	L CTG	V GTA	PCCT	SAGC	R CGC	9 990
L	L	G GGT	S TCC	N AAC	L	S	$_{ m CTT}$
L CTG	A GCG	H CAC	I ATC	N AAC	9 9	A GCG	A GCT
K AAG	R CGC	L CTG	H CAC	H CAC	R CGG	P	P CCA
E GAG	L CTG	H CAC	G GGA	$_{ m L}$	Q CAG	V GTA	A GCC
L	GGC	D GAC	L CTG	Y TAC	H CAC	K AAG	S TCG
A GCG	H CAC	F TTC	R CGG	CIC	W TGG	T T T C	S TCG
G GGG	T T T C	S TCC	N AAC	9 96C	R	A GCC	C TGC
L	A GCC	F	S	N AAC	Q CAG	L TIG	N AAC
9 999	H CAT	S TCG	S TCC	K AAG	L CTA	C TGC	E GAG
D GAC	E GAG	A GCC	CIC	CIC	L CTG	V GTA	H H H H H H
L	D GAC	L	D GAC	FTC	H CAC	Y	V GTC
D GAC	TIC	E GAA	L CTG	A GCC	Y TAC	EGAG	R CGC
H CAC	H CAC	N AAC	TACT	P CCG	L	R CGC	S AGC
R CGC	V GTG	C TGC	H C H	L	R	A GCG	H CAC

Fig. 1B

385 1369 365 1309 425 1489 305 1129 325 1189 405 1429 345 1249 445 549 P QCAG R H CAC FITC P PCCC P TACG E GAG g GGC V GTC S TCC A GCC Q CAG A 3CA S AGC Q CAG GGA Q CAG T ACA T ACC F D SAC T ACC PCCA V GTA N AAC N AAC L N AAC P N AAC A GCG N AAC H CAC F TTC Y TAC P CCA P C TGC R AGG 9 9 9 H CAC A GCT L A GCC T ACA Y TAC CIC I ATA L CTG E GAG L CTG Γ TACC LCTT A GCC RCGC P CCC V GTG P S AGC LCTT AGG E GAG L ITG PCCC E GAG L P L CTC α V GTG Γ L CTG Q CAG S AGC GGG PCCA V GTA S TCC Q CAG GGC PCCG TACT R CGC LCTT S TCA D GAC A GCC R CGG P PCCG GGC C TGC S TCC A GCC A GCC K AAG GGT S TCG L CTG V GTG F TTT L CTG VGTG V GTT A GCC H CAC C TGC H CAC R CGT L CTG W TGG V GTG V GTG VGTG $_{\rm TGT}$ R CGC P A GCG A GCC A GCG F TTC G GGC $_{\rm TGC}$ E GAG S AGC Y TAC I ATT I ATC L CTC V GTG L CTG C TGC A GCT S AGC L CTG RCGC N AAC L CTG R GGC GGA R AGA CAC GGC P CCA M ATG A GCG YTAC T ACA C TGC E GAG D GAT E GAG TACC A GCT A GCC H CAT PCCC

Fig. 1C

S P Q G Q A S T S T * AGC CCG CAA GCG TCC ACA AGC ACG TAG	45 158
rcttrctggagccaggccggagggcctcaatggcccgcgtgcagctggcagtagctgaggaattcgatctctacaacc	166
CTGGAGGCCTGCAGCTGAAGGCTGGCTCTGAGTCCGCCAGCTCCATAGGCTCCGAGGGTCCCATGACAACCTAGACTGC	174
CAGGGCTCCCCCACCCAGGCCCCCCACCCTCTTGCTGCTCGCCCTGCTCCCTGCTTCGGTCCAGAGAACTGGCAGATACT	181
SGTGGGAAGCACTGTGCCTGGCCCCCCCAGCTTCCTGTATGGGCCTCGAAACACAATGGGCCTTCTCGCTCACTGGTAGA	189
SACAGGGGTTGTGGTCCCCCAACCTGCCTTCTGCCCCTGCACAGGACCCAAAGGCCCCCAGGCCCTGCAAGGTGTG	197
CTAGTTCCTGCTTTCCCGGGACTTCCTAGTGCCCAAATGCCCTGTGAGGCTGAGAGACCCAGGCCCCTGTGGGCTTTCA	205
ACACAGCACAGCTGTGGAAGTGGCTGTGTTCTTCTACAGCCTGTGGAAGAACCCCTGTAGCAGAGCAGAGCCTCCCATCCACCC	213
ICAGGGGCTGAGGCAGCTCTCGAGGAGTGGTGCTCAAGAGCTGACGCAGGGCCACCTCCCCTTCCCAAGGGGGTGGGAG	221,
3GAGTGGGCCCACAGGGAAAAGAAGGCGGCTCTGAAGGAAG	229.
CCCCCTCTGGTGAAATGGGACTCCCTCCATCCACCACCCAACCTTCTTGAAAGCTTCACAACTTCACGCAGAGTCC	237
SGTGGCAGGCACCAGGCAGGAAAGGCTCCTCAAGAGGTTCCTGGTGGTCTGGCCTAAGCCCCAGCCAAGAGGCCCTGGCTC	245

Fig. 11

2895 TCTCTGGCCTGGGGCATCCACCCGTTGTTCTGAAGGCAGAGCCCATTCTGTGGGCTCACAAGACACAGTGAAGGGGGATC 2530 CTGGGGGCCCCCCATGGCCATCCTGGACCTCGCTCCAGAGTTTAATAAAGGTAGCACATGCTTATTGCTAGAAAAA 2846 GAACTCCACGTCCCTCGAGAGCAGGAGCCTCTTAAGGGCTGGCACTGGTCTCAGCCTAATGGCTGAGGCGGTACCCTGG 2688

Fig. 1E

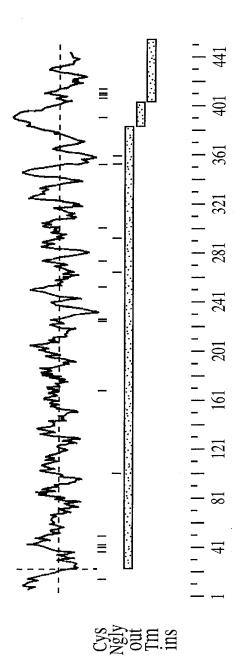


FIG. 1F

70 LSH		3A- LDP	200 ISV .:	FFQH LWEC 260
ADLD]	· 日 · 日	130)L-DGL(:::: LCEGL)	KLGH.	FFQH LWLWEC 260
) PAAT	: CLRTI 60	13 3HDL- • : 13 13	90 DLSSNI .: GLAD190	260 PASRVR- ::::. PASRLK'
60 PAELP	TEL	AALGI · : SDAGI	190 TILDI.:	26 (VPAS ::: :SPAS 250
ODVE	ANPSI 50	120 SNTLF:::DNPLC	SATHLL : AGARVL 0	LAFE
50 GLGI	.: -ALR	110 120 130 SGLRLLDLSSNTLRALGRHDL-DGLGA- . :: :::: : : : : : : : : : : : : : : :	180 HGLS/: IGEAC	250 REYVCLAF : .: AELCPGL
LSCI	:: GS	10 SGLRLI • :: : PTLREI	1 DHLF:	23 RDFARE : SDAGIAI
) :AADI	:. HCKD1 40	110 SG: SG: 	SESE	SAVE
40 KCIC	TEEF	NA STLR	170 180 190 CNELASFSFDHLHGLSATHLLTLDLSSN ::: : ::: :: ::: .:: .:: .:: .:: .:: .	240 QRGLSZ DLGSN(
INCPY	·: DCGI	::. ::. :GVLF	'ALGC	ORWE:
20 30 40 50 60 70 VGLGTPDSEGFPPRALHNCPYKCICAADLLSCTGLGLQDVPAELPAATADLDLSH	: . : .: .: .: .: .: .: .: .: .: .: .: .	90 120 130 QLRALHLDHNELDALGRGVFVNASGLRLLDLSSNTLRALGRHDL-DGLGA::.:::::::::::::::::::::::::::::	150 160 170 180 190 200 HLD-EHAFHGLRALSHLYLGCNELASFSFDHLHGLSATHLLTLDLSSNRLGHISV : ::: :: :: :: :: :: :: :: :: :: :: ::	220 230 240 250 260 YLHNNPLPCDCRLYHLLQRWHQRGLSAVRDFAREYVCLAFKVPASRVRFFQH : : : : : : : : : : : : : : : : : : :
GFPE	·	HNELL · : NCSLT	1 IGLRP:::: :::: VULRP:	2 DCRLY:
PDSE	: LPLLÇ 20	HLLDH : SLQN	HAFHG: PLASV: 160	O PLPC KDLC
20 GLGT	TELL	90 LRAL : IQKL	150 LD-E . :	220 THNNP: : PANCK 210
	: Darw	PLFQ : PTCK 80	RLVH ::. RLTA 150	-GLY
10 TLLC	: EQLS 10	80 GWLA :	140 LEKLLLFNNRLV ::::: :::: QCHLEKLQLEYCRLT 140 150	210 AFLKN : : :
VLLG	DIHC	QRLRP HLVLQ 70	140 LEKLLLI: ::::: LEKLQLE	ALPA .: TLR-
10 MTWLVLLGTLLCMLR	:. : : : : : : : : : : : : : : : : : :	NAL AGV		210 PELAALPAFLKN-GL .:: :::: CQLETLRLENCGL
Ħ	Д	н ч	н а	н с

Fig. 1G

0 280 290 300 310 320	SRVFENCSSA-PALGLKRPEEHLYALVGRSLRLYCNTSV-PAMRIAWVSPQQELLRAPGSRDGSI	DITASGCRDLCRVLQARETLREL-SLAGNRLGDEGARLLCESLLQPGCQLESLWVRSCSLTAACCQHVSL 270 280 330	330 340 350 360 370 380 390 H AVLADGSLAIGNVQEQHAGLFVCLATGPRLHHNQTHEYNVSVHFPRPEPEAFNTGFTTLLGCAVGLVLVL		400 410 420 430 440 450 H LYLFAPPCRCCRRACPLPPLAPNTQPAPRAEPHK-SSVLSTTPPDAPSPQGQASTST	SNNCVGDPGVLQLLGSLEQPGCALEQLVLYDTYWTEEVEDRLQALEG	400 410 420 430 440 450
270	H SRVFENCSS	P DITASGCRDI 270	330 34 H AVLADGSLAJ	 P MLTQNKHL	400 H LYLFAPPCRO	:	400

Fig. 1H

48	9	144	192	240	288	336
tta acc cgc ctg cgg Leu Thr Arg Leu Arg 15	atc tcc atc cct gag Ile Ser Ile Pro Glu 30	ctc tac ctg cac aac Leu Tyr Leu His Asn 45	ctg ctc cgg cgc tgg Leu Leu Arg Arg Trp 60	gaa cgc gag tac aca Glu Arg Glu Tyr Thr 80	cgc ttt ttt gag cac Arg Phe Phe Glu His 95	gct cca ggc tta gag Ala Pro Gly Leu Glu 110
g ggg	a cat His	agg Arg	C C H I S	ttt Phe 75	gtg	gca Ala
ctg Leu 10	aaa Lys	aac Asn	tac Tyr	gat Asp	cga Arg 90	gct Ala
ggt Gly	ctg Leu 25	aag Lys	ctc Leu	cat His	tac Ser	gtg Val 105
cac His	tgg Trp	ctc Leu 40	agc Ser	ctg Leu	gag Glu	tct Ser
ttg Leu	aac Asn	tat Tyr	tgc Cys 55	gcc Ala	tca Ser	tgc Cys
cac His	tac Ser	act Thr	gac Asp	agt Ser 70	gtg Val	aac Asn
aac Asn 5	t Ser	CCa Pro	tgt Cys	ctg Leu	aag Lys 85	aag Lys
ttt Phe	ctc Leu 20	ctg Leu	CCC Pro	ggc Gly	ttt Phe	ttc Phe 100
ctc Leu	gac Asp	gca Ala 35	ctg Leu	cgg Arg	gtc Val	gtc Val
ttt Phe	ctg Leu	gct Ala	ccg Pro 50	cag Gln	ttg Leu	cgg Arg
ccg Pro 1	act Thr	ttg Leu	aac Asn	cac His	tgc Cys	agc Ser

Fig. 11

384	432	480	528	576	624	672
g ctc g Leu	c ccg r Pro	c gct e Ala 160	g cac n His 5	c aac s Asn	g cca u Pro	g ggc 1 Gly
c ctg ag r Leu Ar 5	gtc tc Val Se	agc at Ser Il	a gag ca n Glu Gl 17	cac ca His Hi 190	ccc ga Pro Gl	att gt Ile Va
cag too Gln Ser 125	gcc tgg Ala Trp 140	gat ggt Asp Gly	gtg caa Val Gln	cgc ctg Arg Leu	gct cgc Ala Arg 205	ggc tgt Gly Cys 220
gtg ggc Val Gly	cgg gtg Arg Val	tct cag Ser Gln 155	ggc agg Gly Arg 170	ggg ccc Gly Pro	caa aag Gln Lys	ctg ctg Leu Leu
cg cag la Gln 20	cc act la Thr	sa gcc ro Ala	c ata a Ile	c agt a Ser 185	gt gtg er Val 00	c acc r Thr
cac g His A	cct g Pro A 135	gcg cc Ala Pr	tta gc Leu Al	ctg gc	gtg a Val S	ttt ac Phe Th 215
cag ctg Gln Leu	agt gtg Ser Val	ctt gtg Leu Val 150	ggc agc Gly Ser 165	gtg tgc Val Cys	tac aat Tyr Asn	aca ggc Thr Gly
aa gag lu Glu 15	ac acc sn Thr	ag ctg lu Leu	ct gat la Asp	tc ttt al Phe 180	tt gag eu Glu 95	tc aac he Asn
g cct g u Pro G	c tgc a e Cys A 130	g aat g s Asn G 5	g ttg g 1 Leu A	a ggc g a Gly V	g aca c n Thr L	g act t u Thr P 210
r c Le	tt Ph	aa Ly 14	g t Va	gc	ca. Gli	ga

Fig. 1J

720	768	816	864	912	096
gt ggc tgc rg Gly Cys 240	cc cgg gca ro Arg Ala 255	tt agc act eu Ser Thr 70	ag cat gtg ys His Val	tg cag ctc al Gln Leu	tg caa ctc eu Gln Leu 320
tgt c Cys A	tgg c Trp P	atg Met L 2	cac a His L 285	cgt g Arg V	ggc tt Gly Le
ccc Pro	tgc Cys	tcc Ser	gtc Val	ggc G1y 300	atg Met
cca Pro 235	cgt Arg	tcc Ser	agt Ser	aat Asn	CCC Pro 315
gca Ala	aac Asn 250	cag Gln	gcc Ala	ctc Leu	aac Asn
ttt Phe	cgc Arg	gca Ala 265	aag Lys	ggc Gly	tgc Cys
ttg Leu	tgc Cys	agc Ser	cgc Arg 280	aag Lys	ctg Leu
tac Tyr	gcc Ala	ctg Leu	agc Ser	aag Lys 295	gat Asp
ctc Leu 230	cgg Arg	gag Glu	CCC Pro	ggc $_{ m G1Y}$	tcc Ser 310
ttg Leu	cag Gln 245	cag Gln	gca Ala	ccg Pro	gac Asp
gtg Val	tgt Cys	ctc Leu 260	gat Asp	gag Glu	cca Pro
ctg Leu	tgc Cys	cca Pro	cca Pro 275	ctg Leu	cct Pro
gtg Val	cac His	agt Ser	cca Pro	ttc Phe 290	gta Val
ctg Leu 225	tgt Cys	tcc Ser	acg Thr	gtc Val	gca Ala 305

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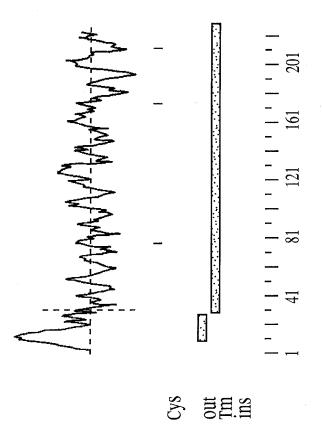


FIG. 11,

Z	\vdash	PFLFNHLHGLGLTRLRTLDLSSNWLKHISI 30
出	151	-
\mathbb{M}	31	PELAALPTYLKNRLYLHNNPLPCDCSLYHLLRRWHQRGLSALHDFEREYT 80
田	201	
Σ	81	CLVFKVSESRVRFFEHSRVFKNCSVAAAPGLELPEEQLHAQVGQSLRLFC 130
Ш	251	
\boxtimes	131	NTSVPATRVAWVSPKNELLVAPASQDGSIAVLADGSLAIGRVQEQHAGVF 180
н	301	NTSVPAMRIAWVSPQQELLRAPGSRDGSIAVLADGSLAIGNVQEQHAGLF 350
\mathbb{M}	181	VCLASGPRLHHNQTLEYNVSVQKARPEPETFNTGFTTLLGCIVGLVLVLL 230
田	351	
M	231	CCHCCQRACRNRCWPRASSPLQELSA.
エ	401	
M	280	RKASVHKHVVFLEPGKKGLNGRVQLAVPPDSDLCNPMGLQL 320
Щ	447	PQGQASTST455

10	30	50 189	70	90 309	110 369	130 429	150 489
L CTG	N AAT	Q CAG	C H	CIT	N AAC	L CTG	A GCC
F TTC	D GAC	L	R CGA	CTT	L CTG) 9	L CTA
L	A GCG	F TTC	CIC	CCT CCT	A GCT	T ACT	I ATC
Q CAG	W TGG	P	CIC	N AAC	V GTG	FIC	9 9 9 9
Y TAC	K AAA	H CAT	Y TAC	T I C	Y TAT	I ATA	L
K AAG	A GCA	Q CAG	F H H C	CC C	M ATG	I ATC	W
TACC	S TCG	H H C	A GCC	Q CAG	L	V GTG	Q CAG
W	CIC	S AGC	A GCT	Q CAG	S AGC	A GCA	S AGC
A GCC	T ACG	H CAC	L CTG	P CCC	TACC	G GGT	L CTG
M ATG	N AAC	E GAG	C TGC	D GAC	G GGG	R CGG	V GTG
GAC	I ATC	K AAG	S	V GTA	T ACA	L	Γ
GTCCGCCGAC	S TCC	S AGC	F TTC	S AGC	M ATG	M ATG	R AGG
	9	GGG	E GAA	S HCC	D GAC	Q CAG	R CGG
CCAG	T ACC	G GGA	G GGA	D GAC	C TGT	FIC	უ ტ ტ
BAACC	V GTT	C HGT	L CTG	S TCA	L	S AGC	L
SGGC	L	GGC	H H H C	Q CAA	A GCG	S	F
GTCC	M ATG	E GAG	M ATG	G GGG	P CCA	A GCC	A GCC
SACGO	CIC	A GCC	G GGC	A GCA	PCCC	S AGT	V GTG
GTCGACCCACGCGTCCGGCGAACCCCAGC	GGG	M ATG	V GTG	A GCT	L	T ACC	S TCG
GTCG	A GCC	H H C	A GCA	R AGA	F TTC	M ATG	F TTC

Fig. 2A

210 669 170 549 190 609 230 250 789 270 849 290 909 310 969 V GTT R CGG M ATG L TTG I ATC TACC L S AGT I ATC L CTG PCCC A GCA N AAC A GCC A GCA D GAC I ATC GGC S AGC PCCA V GTG D GAT L Q CAG L CTG H H CAC EGAG $_{\rm L}$ L CTG S AGC K AAG A GCC E L V GTG L L L S AGC N AAT MATG L CTG T ACA A GCA K AAG A GCA I ATC H CAC L S TCC GGG VGTG T ACC W TGG I ATC L L CIC A GCC V GTC K AAA R CGT I ATC L Y TAC D GAC I ATC PCCT I ATT S AGC V GTC I ATC A GCT L CTG VGTC V GTG N AAC L V GTT 9 9 9 9 L D GAC F TACC FTTT GGA P g GGC ტ ტ Q CAG K AAG 9 96C S AGC A GCA R GGC √ GTG T ACA E GAG F Q CAG F L FTTT V GTC I ATC EGAG L CTC S TCC GGC N AAC S AGC V 3TG V GTG V GTG L G GGC GGC F D 3AC L E GAA Q CAG E GAG A GCC F V GTG L GGG SAGC MATG TACT P CCC C IGC A GCC V GTG A GCG Q CAG I ATC FITC I ATT CIC 9 9 9 0 0 M ATG IATC K AAG I ATC Y TAC S AGC V GTT A GCC R TACC H CAC A GCC A GCA Y TAC D GAC S AGC TACC

Fig. 2B

372 1155 370 1149 1313 330 350 1089 1518 T ACT GGTTCCCTGGAGGCTTCTACTGCCACCCGGGTGCTCCTTCTCCCTGAGACTGAGGCCACACAGGCTGGTGGGCCCCGAA AGCTCTCTGGACCCCTCCTACAGCACTAGAGCTAAATCATGAAGTTGAATTTGTAGGAATTTACCACCGTAGTGTATCTG L CTG CCAAGICCICITITICICACTACCACCIGCAGGGIGGIGITACCCAGCCCCCACAAGCCIGAGIGCAGIGGCAGACCIC A GCC TGCCCTATCCCCAAGGCCTCACCCTGTCCCCTCCCTGCAGAACCCCCAGGGCAGCTGCTGCTGCCACAGAAGATAACAACAC GGC D GAT CCC N AAT I ATA R IATC L CIT . GGC CCC L R AGG T ACT I ATA S R L L CTG CGC L G G T CTG GGT GGC ACC F TTC . GGC G GGC AATCATAAACTAGATTATCATAAAAAAAAAAAAAAAAAGGGGGGCGCCGC L CTG CTT Q I CAG ATC L CTG CIG P L CTG R CGT E Q E R GAG CAG GAG AGA A GCA H CAC $_{
m CTA}$ H CAT F TTC G GGG Y N TAC AAT (E S GAG AGC A GCC E GAG E GAG L A GCA . 667

Fig. 20

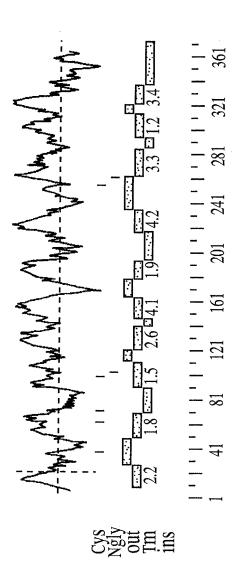


FIG. 2D

5 25 132 45 192 65 252 105 372 85 312 125 432 W TGG FTTC L GGA N AAC L CIG L W TGG TGG R CGG LCTT K AAG Q CAA H CAC A GCC Z H CAC GTG GGG GGG . 966 L CTG ტ ტ S A GCT > P CCA GAG V GTA T ACT E GAG K AAA A GCC S AGT 口 gcc Ø A GCT V GTA PCCC L CTG Q CAG N AAT V GTG ATG . Σ GGG T ACG E GAG I ATC Y TAC A GCC V GTC ᠐ STCGACCCACGCGTCCGCGGGACAGCTGGCTGAAGCTCAGAGCCGGGGGGGTGCGCC I ATT A GCC T ACG E GAG C TGT CCC Y FAC GGC L CTG L CTG M ATG E GAG Q CAG T ACC G L CTG E GAG T ACG S AGC TACT L CTG C TGC 9 96C GGG L CTG K AAG FITC K AAG FTTC WS TCT T ACA A GCC K AAG CGC CCC L CTG S TCT L CTG FILL E GAG I ATC Q CAG R AGG VGTG F TTC L V GTG FTTC F A GCA T ACA D GAC A GCC PCCC N AAC A 3CC A GCA K AAG Q CAG E GAG FTC A GCC Y TAC L CTG R CGT I ATC EGAG R CGA CH TACC LCTG CCG CCG GGC $\overline{\mathbf{W}}$ E GAG A GCC GGC W TGG V GTG TACC 999 S TACC CIGI V GTC CHI Q CAG Q CAG V GTG IATC V GTC A GCT N AAC S TCC Y TAC A GCG N AAC Y TAC

Fig. 3A

65	85	205 672	25 32	244 789	68	947	26	05
H 70	7 0		7	7 2	∞	Q	102	1105
G GGC	C HGC	T ACC	T ACA		CTT	GTG	4AGG	CTC
C TGT	T ACA	M ATG	S TCA	* TGA	GCAC	GGT	CTG2	ACAC
G GGA	R AGA	P CCT	P H ; cca cac	P CCA	GTG	AGCP	GTTC	CAGG
8 E E	L	V GTC	P CCA	T ACT	GAGT	೨೦೦೨	CCAC	CCTG
T ACT	V GTC	S AGT	R CGG	TACC	CTGA	CTAT	TGGA	ACAC
L W CTC TGG	L S V L	A S V GCA AGT GTC	C T R TGT ACT CGG	CCC	GTAC	ACTG	GAAG	ATGC
CIC	CIC	R AGG	C TGT	GGC	CTAT	TCCG	AGAG	9299
L CTT C	S TCT	G R GGA AGG	V S GTG AGC	W TGG	CTGC	GGAG	CTGC	TGCA
TACC	T ACC	M ATG	V GTG	T ACA	GGCT	CAGT	GACC	CAGC
L	I ATC	K AAG	M ATG	V GTA	TGTA	9992	CACG	CAAC
L L T CTC CTC ACC	L I T CTC ATC ACC	$_{ m L}^{ m L}$	W	C HGC	ACTT	GGAG	5255	ACTT
A GCC	L	S L K M AGT TTG AAG ATG	L TIG	S C V T W G P T T P TCC TGC GTA ACA TGG GGC CCC ACC ACT CCA	.CGAACCTCACTTTGTAGGCTCTGCCTATGTACCTGAGAGTGTGGGCAGCTT	TTCTTCAGGGAGCGGGCAGTGGAGTCCGACTGCTATGCCGAGCAGGTGGTG	ATATGGGGGGGCGCACGGACCCTGCAGAGGAAGTGGACCACGTTCCTGAAGG	GCAGCTCTACTTCAACCAGCTGCAGGCGATGCACACCCTGCAGGACACCTC
CCC	H CAT	E GAG	F	L TTA	CGAA	TTCI	ATAT	GCAG
CCC	K AAG	M ATG	A GCC	P CCA	TCAA	CTTC	9299	ACTG
Q CAG	CTT	S AGC	$_{ m CTG}$	N AAC	TGGC	TCTA	CAAG	CCGA
CCC	A GCC	M Teg	M ATG	CGG	CTTT	AAGG	TCTG	TGCC
C TGT	PCCT	L	A GCC	A GCA	TGGC	CGAC	CGTG	GCTC
R CGG	S AGC	S TCA			AGACAGAGTACCTGGCCTTTTGGCTCAA	CACGGGGGACGACGACAAGGTCTACTTC	GCTCGTGTGGCCCGTGTCTGCAAGGGCCG	CGCGGCTGGCATGCTCTGCCCCGAACTG
CCT	Q CAG	P CCT	L R CTA AGG	T S W ACT TCC TGG	AGAG	9999;	GTGT	GCTG
L CTA	P CCA	S TCA	Q CAG	T ACT	AGAC	CACG	GCTC	5252
						e e o períodició Compresenta		

Fig. 3F

1263 1816 1895 CTGGCACACACACCTTCTTTGGGGTTTTTCAAGCACAGTGGGGTGACATGTACCTGTCGGCCATCTGTGAGTACCAG 1184 ACCCTGTACCCAGGCCCTGGTTGTGATGGCTGCCCCAGCCCCGCCATGCCGGGGCCTACCACTGCTTTTCAGAGGAGCAG 1342 CCCAAGGAGCCCACCAGTCCCCCTTCCGGCCCTGTCCTGAACCAGAAGCTTTGGGATCCTGTCGGTTACTACT 1658 ATTCAGATGGCTCCCTTAAGATAGTACCTGGGCATGCCCGGTGCCAGCCCGGTGGGGGGCCCCCTTCGCCACCTCCAGG 1737 TGCAGCAACGCCAGCCACTGCCCGACTCCAACCCCGAGGAGTCATCAGTATGAGGGGAACCCCCACCGCGTCGGCGGA 1974 GGGGCGCGCGCTGCTGCTGAAGGCTACCTTGTGGCTGTCGTGGCAGGCCCGTCGGTGACCTTGGAGGCCCGGGCCCCCC 1421 ATTGCGCCGGCGGCTGCGGGAAGAGCTGGAGAAAGGGGCCCAAGGCTACTGAGAGGACCTTGGTGTACCCCCTGGAGCTG TIGGAAGAGACCCAGCGGGTGTTTGAGGGCCCCCTATAAGGAGTACCATGAGGAAGCCCCAGAAGTGGGACCGCTACACTG

Fig. 3C

2448 2290 2369 2527 2606 GCCCCGGGGGTTCAGTGGTATTTTATACTTGCCTTCTTCTTGTACAGGGCTGGGAAAGGCTGTGTGAGGGGAGAGAAGGG 2685 GACAGATACTGCCCAGCACCCACCGGCCATGAGGACCTGCTCTGCTCAGCACGGGCACTGCCACTTGGTGTGTGGTCTCAC 2132 2811 CTATGAAGGGGAAGGGGTCGTATCACTTTGTCTCTCCTACCCCCACTGCCCCGAGTGTCGGGCAGCGATGTACATATGG AGGTGGGGTGGACAGGGTGCTGTGCCCCTTCAGAGGGAGTGCAGGGCTTGGGGGTGGGCCTAGTCCTGCTCCTAGGGCTG GCGTGCGCGCTTGTGGCATAGCCTTCCTGTTTCTGTCAAGTCTTCCCTTGGCCTGGGTCCTCCTGGTGAGTCATTGGAG CAGGGCACCAGCCTCGCAGAAGGCATCTTCCTCTCTCTGTGAATCACAGACACGCGGGACCCCAGCCGCAAAACTTT AGAGGGTGGGCCTGCTGGACAATGGCATACTCTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTGTAACTTATTGT GTCCCCGCGTATTTATTTGTTGTAAATATTTGAGATTTTTATATTGA

Fig. 3L

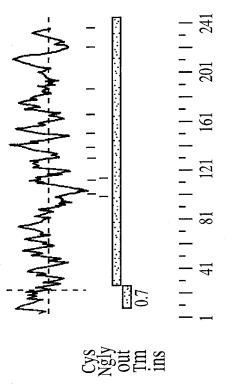


FIG. 3E

Σ Ξ	10 20 30 40 50 60 70 MAPHWAVWLLAAGLWGLGIGAEMWWNLVPRKTVSSGELVTVVRRFSQTGIQDFLTLTLTEHSGLLYVGAR ::::::::::::::::::::::::::::::::::::
Σ Ξ	80 100 110 120 130 140 EALFAFSVEALELQGAISWEAPAEKKIECTQKGKSNQTECFNFIRFLQPYNSSHLYVCGTYAFQPKCTYI ::::::::::::::::::::::::::::::::::::
∇	150 160 170 180 190 200 210 NMLTFTLDRAEFEDGKGKCPYDPAKGHTGLLVDGELYSATLNNFLGTEPVILRYMGTHHSIKTEYLAFWL
田	
Σ Ξ	220 230 240 250 260 270 280 NEPHFVGSAFVPESVGSFTGDDDKIYFFFSERAVEYDCYSEQVVARVARVCKGDMGGARTLQKKWTTFLK :::::::
Σ Ξ	290 340 350 350 350 350 340 350 and arlucsapdwkvyfnqlkavhtlrgaswhnttffgvfqarwgdmdlsavceyqleqiqqvfegpykeyse : : : : : : : :

Fig. 3F

420 VKKNTNF . :	490 LFAGSRS SVPMT	560 YGIKKVR	630 GPYRCYS	700 ELEKGAK
410 KPRLGRPLI :: LL	480 PVESLVLSQSKKV:: SMESLKMGRA	550 LDTSKMCNQ	620 MAAQSRHS	690 SIRRRIRE:
370 380 400 420 PGSCINNWHRDNGYTSSLELPDNTLNFIKKHPLMEDQVKPRLGRPLLVKKNTNF :: :: :: :: :: :: :: :: :: :: :: :: ::	470 LQVFDQEPVES1 :	510 520 530 540 550 560 VDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMCNQYGIKKVR : : : : : : : : : : :	220 590 600 610 620 630 AHAHWTFGSQDLPAEQPGSFLYDTGLQALVVMAAQSRHSGPYRCYS:	680 SAVCLVLLLLVI :
390 LELPDNTLNF	460 .: .: .SLW	20 530 WNVNTSRCVATTSGR: ::: .::) 600 DLPAEQPGS1	670 SLVWLAVVAL(
380 HRDNGYTSSL : SPAL 170	450 DGWLLKAVSLGPW .:.::.:	520 PYCAWNVNTS : :	220 590 AHAHWTFGSQ :	660 EARAPLENLG :::: -ARNPLS
370 PRPGSCINNW ::	'440 TYTVLFIGTG	510 FCVDCVLARD : : FL	580 PCHLSSNI	650 AVVAGSSVTL
360 M QAQKWARYTDPVPSPR ::: HWTR	430 450 460 470 490 490 490 490 A 90 400 470	500 QLVQLSLADCTKYR :: .:: QLRAM-LA	210 570 M SIPKNITVVSGTDLVL H	640 650 670 680 690 700 M EEQGTRLAAESYLVAVVAGSSVTLEARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRLREELEKGAK :::: HCVT230
← 4	4 47	N H	Z H	Z H

Fig. 3G

770	SIPGQP		1				
. 760	PGGGPPSPPC	•••	GPTTP	240	830	PDSNPEESSV	
750	ASPPFRPGPETDEKLWDPVGYYYSDGSLKIVPGHARCQPGGPPSPPPGIPGQP				820	LRRKLQQRQPI	
740	PVGYYYSDGS		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		810	SHPLPELADE	
730	PETDEKLWDI	••	M		800	LGGEDRGGS	1 1 1 1 1
/20	EPASPPFRPG				790	SNANGYVRLÇ	
01/	M ASERTLVYPLELPKEP				780	M LPSPTRLHLGGGRNSNANGYVRLQLGGEDRGGSGHPLPELADELRRKLQQRQPLPDSNPEESSV	
	M		Н			\mathbb{Z}	

Fig. 3H

Fig. 31

420 CAG ::: CAG	490 CCT :::	560 GGA	630 TAC :	700 CCA
ACC ACC	cac	GAG	TGT	CIC
3CA	.: .: .: .:		1 PGC	CA
0 AGAG AGAZ 370	TGC::TG1	AAT	TG2	cac :::
410 GAA ::: GAA	480 GTC GTC GTC	550 CAG : C	620 630 GGACGGTGAGCTGTAC :: :	690 ACCCA ::::
, , , , , , , ,	ATC:	5. GTGC/ GTGC/ GTGC-	GAC	-55 -55 -559
4.4.4 4.4.4.	1 1		GTG I	690 ATGGGGACCCACC ::::::::: ATGTGG-CCCAC- 550
;3AG; ;3: ;3AG;	TIC.	GA(EH I	ICA!
400 CCC ::	470 CCA: CCA(540 TTGG/ ::- -TGA-	610 CTCCT :::	680 ATA
5TA :::	C :: C	ACC -	3AC	901
ATC .:.)) [] []	TCZ	CCGG : CCAG	CTJ
0 TGA ::: TGA	0 AAT AAT 420	1 H	590 600 ACCCAGCTAAGGGTCACACCGGA :: :: :: ::: -CCTACCTCGGTGTC-C-CCAGC 500 510	O A T C
390 AATT : :	460 ACA	530 CAC	600 CAC :- :	670 TTA:
AAP ::. AAG	CAI : : CCI	GCT	6GTCZ :::	990
14G :::	4GC	3AT	TAAGG:::TCGGT500	7
0 AG2 AG2 34(50 TTC? : :: TGC?	0 AAC	590 AGCT/ ::: ACCT(5(O AGZ GTC
380 31GA :: 1GGA 3	45 300 T T T T T T T T T T T T T T T T T T	520 ATCA :::	590 CAGC	660 CACA :::: CTCG
AG('ACZ ::	$\mathcal{G} :: \mathcal{G}$	
		510 520 GTGCACCTACATCA ::::::::::::::::::::::::::::	TGA	D D
33.0	10 11C(11C(40)	0.0 3.0 4.7.0 4.7.0	NTA'	00
370 GAGG :::: GAGG	440 TCAT :::: TCAT	510 GTGC :::: GTGC	580 CCAT:::::	650 ACTT .:: TCT-
 	4CT	CAA :::	ATGCCI-	ATA T 530
	CAZ CAZ CAZ	500 GCCTTCCAGCCCA :::::::::: GCCTTCCAGCCCA	AA	CAZ ::
360 ATCT :::: ATCT	430 GCTT :::: GCTT	500 CCAG :::: CCAG	570 GGTA	640 CACT
3. ::: GA!	4 H	. H . H . D . D . D . D . D . D . D . D	. 2	ACL TC
75 5 75 5 75 5	3AB :::	0 ·· 0	GAP	00 :: 00 10 :: 00
360 370 380 400 410 420 AGGAGCGAGCTCCAGCTGAGAAAATTGAATGTACCCAGAAAGGGAAGACCAG :::::::::::::::::::	430 440 450 460 470 480 490 ACCGAATGCTTCAACTTCCTTCTTCAGCCATACAATTCCTCCCATCTGTATGTCTGCGGCACCT ::::::::::::::::::::::::::::::::::	500 510 520 I ATGCCTTCCAGCCCAAGTGCACCTACATCAGAGTGCACCTTCCAGGCCCAAGTGCACCTACGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGACCTACGTCGAGGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCAGAGTCGAGGTCGAGTCAGAGTCGAGTCGAGTCAGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCAGAGTCGAGTCAGAGTCGAGTCGAGTCAGAGT	570 580 610 TGGGAAGGGTAAATGCCCATATGACCCAGCTAAGGGTCACCGGACTCCT :::::::::::::::::::::::::::::::::	640 650 700 700 700 700 680 690 700 700 520 700 7200 7200 7200 7200 72
360 370 380 420 400 410 420 M AGGAGCGATCTTGGGAGGCTCCAGCTGAGAAAATTGAATGTACCCAGAAAGGGAAGAGCAACCAG :::::::::::::::	430 440 450 460 470 480 490 M ACCGAATGCTTCAACTTCCTTCTTCAGCCATACAATTCCTCCCATCTGTATGTCTGCGGCACCT ::::::::::::::::::::::::::::::::::	500 510 520 530 540 550 560 M ATGCCTTCCAGCCCAAGTGCACCTACATCAACATGCTCACGTTCACCTTGGACCGTGCAGAATTTGAGGA : ::::::::::::::::::::::::::::::::		M T H C

Fig. 3J

770 STGAGAG	: :: -TTAGA-	840 GTATGAC ::::: GTTTGA- 640	910 CACGGACGC : :: : CTATGACCC 670	980 TCTACTT ::: -CAACAA 730	1050 GGGTTTTT :
760 CTTTGTCC	:::: ::::: CTCTCTCTGTCC-' 590 600	830 GCAGTGGAGTATGA .: .::::::::::::::::::::::::::::::::::	900 GGGGAGCA(::	970 ACTGGAAGG:::	1040 CTTCTTCGG(::::CTGCG760
750 TAGGCTCTGC	 	820 CAGTGAGCGG .::::- -TG-GAGCA-	890 GGTGACATGG	960 CTCAGCCCCTGA ::::::::: CTCGGCCACA	1030 CAACACCAC
740 SAACCCCACTTTG	:.: ::.:. -ATCTCCTCATCAC 580	820 ACAAGATCTACTTCTTCAGTGAGCGG :::::::::::::::::::::::::::::::::	870 880 890 900 910 CGTGTGGCGAGAGTCTGTAAGGGTGACATGGGGGGAGCACGGACGC : : : : : : : : : : : : : : : : : : :	950 3GGTTGGTGTGCT : .:.:: 3GTGAGCTGTACT 710	10 1020 1030 CGGGGCGCCTCTTGGCACACACACACACACACACACACAC
730 FTGGCTGAAT		800 SATGACAAGAT :::: ACATGCT	870 CTCGTGTGGCGAGAGTC ::::::::::::::::::::::::::::::::::::	940 CCTGAAGGCT(: :: :: : CTTGT-GGAT(1010 acccrgcggggc ::::: cggaac
720 ACCTGGCTTT	::.:: :: ::.:: - AGAGCCCTGCCCTTAAGC 560 570	790 ACGGGAGACC	860 :::::: AGATGG	930 3. : : : : : : : : : : : : : : : : : : :	1000 AGGCGGTGCACZ ::: -GGCA
710 720 730 740 750 760 770 770 760 770 760 770 760 770 760 770	::. AGAG	780 810 820 840 TGTGGGAAGCTTCACGGGAGACGATGACAAGATCTACTTCTTCAGTGAGCGGGCAGTGGAGTATGAC ::::::::::::::::::::::::::::::::::::	850 TGCTATTCCGAGCAGGTGGTGGCT:::::	920 930 940 950 960 970 980 TGCAGAAGAAATGGACGACGTTCCTGAAGGCTCGGTTGGTGTGCTCAGCCCCTGACTGGAAGGTCTACTT .::.:::::::::::::::::::::::::::::	990 CAACCAGCTGA :.:::: CTTCCTG
\boxtimes	Ħ	N H	M H	В Н	Z H

Fig. 3K

1120 GTGT	1190 CCAG .:	1260 GCCG .: AC	1330 CGCC	0 0 U
1. PAG:	1.7 4CCC	12 CTGC : .: CGAC 880	13 2000	1400 ATGGTGC .:: :: GTGTGGC
AGC. : A	GGTA:::	GGAAC ::::: GGGAC 8	999	GAT
.10 .TCCA(.:::	30 CCC(CTTT	1250 CCCTGGAACTG : :::: . -CGGGGGACGA	20 3GTT	00 3CTT
1110 AGATC	1180 CTGACC :: :: CTCACT	1250 rcccr : cgg	1320 CTCGG' : ::. C-CGA	1390 1666C
1070 1080 1090 1100 1110 1120 ATATGGACCTGTCTGCAGTTTGTGAGTACCAGTTGGAACAGATCCAGCAAGTGT :::::::::::::::::::::::::::::::::	Ä Ö	1230 1240 1250 1260 CCGAGACAATGGCTACACTTCCCTGGAACTGCCG :::::::::::::::::::::::::::::::::::	D E	1340 1350 1360 1370 1380 1390 1400 CCCTACTTGTGAAGAACACTTCACACACGTGGTGGCCGACAGGGTCCCAGGGCTTGATGGTGC :::::::::::::::::::::::::::::::::
0 TGG	0 CTAT: : :. CGAA 820	0 ACCA ::: TTCA	310 GGTGAAG .::::: AGTGGAG 920	0 GGTC 1: 950
1100 AGTT:	1170 CCGCT : .: CAACG	1240 GGCTACAC ::::. GGCAGCTT	1310 .AGGT(.:: -AGT(1380 CAGG
1 1ACCA 1::: ACCA 780	GGG:	.:: 555	36ACC :::: 36GC-	CGA(
3AGT) \GTGG ::: !TTGG	AAT GÍG	0 GAGGACC ::: GGGC- 910	0 TGGC TGGC
1090 TGTG	1160 AGAAG 	1230 1240 CGAGACAATGGCTACACCAG ::: ::::-:::::::	1300 ATGG	1370 GTGGT(:::::
THE	3 : C C 7	3CGZ ::	TGA	1 CGT ::
GCA(O CAAGCC::: CTGGCC	3CAC	, גממ	:: .:: 1GCA(
1080 GTCT(::	1150 GAGC	1220 CAACTGGCA(:::- CTGA 850	1290 GCAC(::	1360 1370 AACTTCACACACGTGGTGGCC: :::::: TGCCGAGCAGGTGGTGGC-
CC	GT G.	12 CAAC : : C 850	12 GAAGC : . : : : GGAGC	13 AACTI : IGC
GAC :	::: ::: TAC 800	CAA(AAG.	CTAZ
1070 ATATG	1140 GGAGTACA ::::: -GAGTAC- 800	1210 TGTATC:::::	1280 12 TCATCAAGAAGC::::: TCTTCAGGGAGC	50 ACA(
10 GAT	11 AGG G	1210 CCCTCGGCCTGGTTCGTGTATCAA: ::::::::::::::::::::::::::::::::	128 TTCA:::TTCA	1350 AGAAC
0 TGGGGC :::::: TGGGGC	TACAA ::: -ACA-	TTC	TCAAC .:.: ACTIC	AGA
1060 CAAGCGCGATGGGGCG :: :::: CATGGGGC-	30 30 1)0 %TGG ::	1270 GACAACACCCTCAACT ::::: : :::: GACAAGGTCTACTTCT	0 TGA
1060 3CGAT	1130 3GTCC	1200 CTCGGCCTG :: :::: -TCTGCCTA 840	1270 CACCC':	1340 CTACTTGT: ::::: CTGCTA 930
AGC(TTGAGG	1 CTCGG::::	sacaac ::::: sacaac	13 CTACTT ::.:: CTGCTA 930
CA.			GAC ::: GAC	: CCC
Σ H	五 田	M H	M H	M H

Fig. 3L

1460 1470 GCCTGGGGCCCTGG : :::::CGGACCCTG-	1540 CAGAGCA : : : : : : : - CTG-GCA	1610 AAAGTACCG .: :: GGCG 1080	1680 3: :: :: :: :: :: :: :: :: :: :: :: :: :	1750 AAGATGT .::.
1460 GAGCCTGGG:::	1530 :GTGCTGTCT ::::	90 1600 TGGCCGACTGCACAA .:::: ACCAGCTGCA	0 1670 1680 GTCAACACCAGCCGCTGTGTG ::::::::::::::::::::::::::::	1740 3GACACTTCAA :.: -GGC-CATCTG
1450 CTGAAGGCTGT ::GCA	1520 1530 1540 GGAAAGTCTGGTGCTGTCTCAGAGCA ::::::::::::::::::::::::::::::::::::	1590 GTCTCTGGCCG ::::. -TCAACCA	1660 CCTGGAATGTCAA ::::::::::: CCTGGCACAA 1110	1730 GGCGAACTTG : .:: ACCTGTC
1440 GCTGGCTGC:::::::	1510 GGAGCCAGT : ::: CGTTCCTG	1580 'GGTTCAGCTGT : ::.:: : 'G-CTCTACT-7	1650 166 ACTGTGCCTGGAAT :::::	0 1720 1730 1740 TCTGGTCCAACATGTGGCGAACTTGGACACTTCAAA ::: .::::::::
1420 1430 1440 1450 1460 1470 TTCATTGGTACAGGAGATGGCTGGCTGCTGAGGCTGTGGGGCCCTGG :: :: :: :: :: :: :: :: :: :: :: :: ::	1500 1510 GGTGTTTGACCAGGAGCCAGT ::: :::::-:	1570 TCTCAGCT .:: .::. ACT-GGCA	1630 1640 1650 1660 1670 1680 GTCCTGGCCAGGGACCCTTACTGTGCCTGGAATGTCAACACCAGCCGCTGTGTG ::::::::::::::::::::::::::::	1710 CCTTTCTGGT(::: GGT:
1420 GTTCATTGGT ::.:: CAAGGG-	1490 GAGGAACTGCAGG :::::: GAGGAAG	1560 CTGGCTCCCGC ::::: GC-CCCGA 1050	1630 rgrccrggcc ::::: cccrgc	1700 171 GCTCGGGGTCCTT::::::::::::::::::::::::::
1410 CACCTAIACAGIGIIG : : .:: CCGIGICIG	1480 1530 1540 ATCCACATGGAGGAACTGCAGGTGTTTTGACCAGGAGCCAGTGGAAAGTCTGGTGCTGTTCTCAGAGCA :: ::::: ::: ::::::::::::::::::::::::	1550 AGAAGGTGCTCTTTGC:::::	1620 TTTCTGTGTAGACTGT ::::::	1690 1700 1710 1720 1730 1740 1750 GCCACCACCAGGGTCGTCGTTTCTGGTCCAACATGTGGCGAACTTGGACACTTCAAAGATGT :
M CA	M AT H	M AG H	M TTTC' ::: H ATGC	M GCO H GTI

Fig. 3M

1890 ACCTGCCT ::-	1960 ACAGTCCC ::: ::: CCAGCCCC	2030 :ACCTTGT :::::: FACCTTGT	2100 :TCGTGTGG : ::::: :TGGTGTGG
1880 GGAAGCCAGG::::::: GGAAGC	1950 IGATGGCCGC :::::::: IGATGGCTGC	2020 TGCAGAAAGCT ::::::: TGCTGAAGGCT	2090 AACCTGGGGCT :::::::: AACCTGGGGCT 1430
1870 .CTGGACCTTC . :: -ATGA	1940 GCGCTGGTGG ::::::: GCCCTGGTTG 1280	2010 CAAGACTGGC : ::::: CGCGGCTGGCT	2050 2060 2100 CTCGTCGGTGACACTGGAGGCTCCCTTGGAAACCTGGGGCTCGTGTGG ::::::::::::::::::::::::::::::::::::
1860 CCCATGCCCA .::: AGTACC	1930 3GGACTCCAG : :::: FGTAC-CCAG	2000 SAGCAGGGGA ::::::::: SAGCAGGGGG	2070 ;AGGCACGGGC :::::::::::::::::::::::::::::
1850 CCAATTTGG(::::: CCTATAAGG/	T.A.	1990 TATTCAGAGG :.:::::: TTTTCAGAGG 330	2060 GTGACACTGGZ :::: :::: GTGACCTTGGZ
		1980 CTATCGTTGC ::::::::::::::::::::::::::::::::	2050 2 CGGCTCGTCGGTGAC ::::::::::: AGGCCCGTCGGTGAC 1390 1400
1830 GGTCCTACCC	1900 GCAGAACAACCTG : :::: GAAGTGGGACC		2040 M TGCTGTCGTGGCCGG ::::::::::::::::::::::::
	1840 1850 1860 1870 1880 TGCCACCTCTCGTCCAATTTGGCCCATGCCCACTGGACCTTCGGAAGCCAGGACC :::::::::::::::::::::::::	1830 GGTCCTACCCTGCCA :::GCC- 1900 GCAGAACAACCTGGC :::.:::::	1830 GGTCCTACCCTGCCA :::GCC- ::::::::::::::::::::::::

Fig. 3N

2170 ccGGCGAC ::::::: ccGGCGGC	2240 CTGCCCAA :::::: CTGCCCAA	2310 TCGGGTAC :::: ::: TCGGTTAC 1650	2380 GCCCCCTT ::::::: GCCCCCTT	2450 GGTCGGAA :: :::: GGGCGGAA 1790
2160 TATCGCTCCG :.::: :: TGTCATTGCG 1500	2230 ccccTTGGAA :::::::: ccccTGGAG	2300 GGGATCCTG :::::::: GGGATCCTG	2370 CTGGGGGTGG : :: :: :: CCGGTGGGGG	2440 CCTAGGAGGT :::::::: CCTGGGGGGGT
2120 2130 2140 2150 2160 2170 CTGGGGGCTGTGCTGCTGCTGCTGCTCCTATCGCTCCGCCGGCGAC ::::::::::::::::::::::::::::	2220 CACTGGTGTA(: :::::: CCTTGGTGTA(2260 2270 2280 2290 2300 2310 cccccccccccccccccccccccccccccccccccc	2330 2340 2350 2360 2370 2388; !TCTCTCAAGATTGTGCCTGGTCACGCCCGGTGCCAGCCTGGGGGTGGGCCCCCTTTAAGATAGTACTGGGGCATGCCCGGTGCCAGCCCGGTGGGGGGGCCCCTTAAGATAGTACTGCCCGGTGCCGGTGCCAGCCCGGTGGGGGGCCCCCTTAAGATAGTACTGCCTGGGCATGCCCGGTGCCAGCCCGGTGGGGGGGCCCCCTTAAGATAGTACTACTGCCCGGTGCCGGTGCCAGCCCGGTGGGGGGCCCCCTTAAGATAGTACTACTAGTACTAGTACTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTACTAGTAA	2400 2410 2420 2430 2440 2450 TACCTGGCCAGCCTCTGCCTTCTCCAACTCGGCTCCACCTAGGAGGTGGTCGGAA : ::::::::::::::::::::::::::::::::
2140 GGTGCTGCTGC ::::::::: GGTGCTGCTGC 1480	2210 TCTGAGAGGAC .::::::::::::::::::::::::::::::::::::	2280 CGAAACTGAT ::: :::: TGAACCAGAT 620	2350 :TGGTCACGCCC ::::::::::::::::::::::::::::::::	2420 CTTCTCCAAC ::::::::::::::::::::::::::::
2130 CTGTGTGCCTG :::::::::: CTGTGTGCCTG	2200 TGCCAAGGCAT ::::::::::::::::::::::::::::::::::::	2270 GTCCTGGCCC : :: :: GGCCCTGTCC 610	2340 GATTGTGCCT ::::::::::: GATAGTACCT 680	2410 CCAGCCTCTGC ::::::::: CCAGCCTCTGC 1750
2120 GCCCTGGGGGC :::::::::::::::::::::::::::	2190 TAGAAAAGGGT :::::::::::::::::::::::::::	2260 CCCCCTTCC:::::: CCCCCCTTCC 600	2330 SCTCTCTCAA :::::::::::::::::::::::::::::::::::	2400 CATACCTGGC :::::::: CATCCCAGGC
2110 2120 2130 2140 2150 2160 2170 CTCGCTGTGGTGCCCTGGTGCTGCTGCTGCTTCGCTCCGCCG	2180 2230 2240 TTCGAGAAGAGCTAGAAAAGGGTGCCAAGGCATCTGAGAGGACACTGGTGTACCCCTTGGAACTGCCCAA :::::::::::::::::::::::::::::::::	2250 GGAGCCTGCCAGTCCC ::::::::::: GGAGCCCACCAGTCCC 1590 1600	2320 2330 2340 2350 2360 2370 2380 TACTATTCGGATGCCTCTCTCAAGATTGTGCCTGGTCACGCCCGGTGCCCTGGGGGTGGGCCCCCTT ::::::::::	2390 2400 2410 2420 2430 2440 2450 ccccacctrgGcCarcacctrgGcCarcGcTrGGCTrGGCAACTCGGCTrCCACCTAGGAGGTGGTrGGAAAAAAAAAA
Z H	N H	Z H	Σ н	M H

lig. 30

2460 2470 2480 2500 2510 2520 CTCAAATGCCAATGGTTATGTGCGTTTACAGTTGGGCGGGGGACCGAGGAGGATCTGGGCACCCACTG ::::::::::::::::::::::::::::::::::::	2530 2540 2560 2570 2580 2590 CCTGAGCTCGCGGATGAATTACGACGGAAACTACAACAGGGCCGCCGCTGCCTGACTCCAACCCAGAGG :::::::::::::::::::::::::::	2600 2610 2620 2630 2640 2650 AGTCTTCAGTATGAGGGGACCCCCCCCCCCCCTCATTGGCGGGGGGGG	30 2670 2720 CTTTTGCACGGCACCTCCTCGGGACATGGCAGGGGCACTTGCTCTGCCTGGGACAGACA	0 2740 2750 2760 2770 2780 2790 catcatttgccccgccgtgacgacctccrcccacctcacct
2460 M CTCAAATGCCA/ ::::::::: H CTCAAATGCCA/ 1800	2530 M CCTGAGCTCGCC ::::::::::: H CCTGAGCTCGCC	2600 M AGTCTTCAGTATGAG ::::::::::::: H AGTCATCAGTATGAG 1940 195	2660 2670 M CTTTTGCACAGG ::::::::::::::::::::::::::::::::	2730 2740 M CATCATTTGCCC :::: H CAGCACCCACCC

Fig. 3P

2800 2810 2820 2830 2840 2850 2860 ACTTCAGCCTCACAGGAGACA-CACCCTCCTCTGTGAATTTGAGACATGTGGGACCCCAGCAGCCAAA :::::::::::::::::::::	2870 2880 2890 2900 2910 2920 ACTITGCAAGGAAGAGTITCAAGAIGIGGGGGGGTTITGTGCATATAIGIGIAGGTAIGCAIGIGGAA :::::::::::::::::::::::::::::::	2950 2960 2970 2980 2990 TGTGTG	3020 3030 3040 3050 3060 GTCTTTGGAGCTATGAAGGGGGTCATAGCACTTTGCTTCTCCTACCCCC :::::::::::::::::::::::::	3090 3110 3120 3130 TGGGGCAGTGATGTACATACGGGAAGGGAAGGACAGGGTGTTGTACCCCTTTTG : ::::::::::::::::::::::::::::::::
0 2820 GAGACA-CACCCTCCTCT .:.:::::::::::::::::::::::::::	2880 2890 GGTTTCAAGATGTGGG :::::::::::::::::::::::::::::	2950 TGTGTGTGTGTT ::: :::: CGTGCGCGCTTGTGGC 2300	3020 TCTTTGGAGCTATGA ::::::::::::::::::::::::::::::::::	3090 TGGGGCAGTGATGTAC::::::::::::::::::::::::
2800 2810 ACTTCAGCCTCACAGGA .:.::::::::::::::::::::::::::::::::	2870 28 ACTTTGCAAGGAAGAGG :::::::::::::::::::::::::::	30 2940 GAATGTGTGTGTGTGT :.::::::::::::::::::::::::	3010 TCCTCCTGGTTGA ::::::::::::::::::::::::::::::::	3070 3080 AGCTGTCCCAAGCTTTC : :: :: :: : A-CTGCCCCGAG-TGTC
м А н С.	M A(: H A(2%	2930 M G2 H G2	M G G G	M A(H A·

Fig. 3Q

3160 3170 3180 3190 3200 CGGGGGTGGGCCTAGCCCTGCTCCTAGGGCTGTGAATGTTTTCAGGGCGGGGTT :::::::::::::::::::::::::::::	3210 3220 3230 3240 3250 3260 3270 GGGGGTGGAGATGGAACCTCCTGCTTCAGGGGGAGGGGTGGGCCTCCCCACTTGCCCTCCGGG ::: ::::::::::::::::::::::::::::::	3280 3330 TTCGGTGGTATTTTATATTTGCGCTCTTC-TG-ACAGGGCTGGGAAGGGTTGTTGGGGGAGGGAAGGG ::::::::::::::::::::	3360 3370 3380 3390 3400 TATGGATACTGGCCTATCCTCCCTGCTCTGGGAAAGGGCTAACAGTGTA :::::::::::::::::::::::::::::::::	3430 3440 3450 3460 3470 ACATATTTATTTGTAAATATTTGAGTATTTTATATTTGACAAATAAAT
3180 CTCCTAGGGCTG C::::::::::::::::::::::::::::::::	3240 3250 GGAGGGTGGGCAG :::::::::: GGAAGGGTGGGTGG	3310 TG-ACAGGCTGGGAAGGG:::::::::::::::::::::::::	3380 TCCCTGCTCTG::::::::::::::::::::::::::::	3430 3440 3450 3460 ACATATTTATTTGTTGTAAATATTTGAGTATTTTTATATTGAC .:.::::::::::::::::::::::::::::::::::
3170 3CCTAGCCCTGC 3CCTAGTCCTGC	3230 32 TTCAGGGGG ::::: GTGTTTGGGGGG	3300 SCTCTTC-TG-ACF ::::::::::::::::::::::::::::::::::::	3370 IGGCCTATCCTC ::: :: ::: IGGCATACTCTC	3440 ITTGTTGTAAAT::::::::::::::::::::::::::::
O I	220 3. GGAACCTCCTGC :::::::::: GGAGCCTCCTGTG' 560 2570	3290 "TTATATTTGCGC" ::::::::::::::::::::::::::::::::::	3360 SCTATGGATACTO ::::::::::::::::::::::::::::::::::::	3430 CCACATATTTAT' CCGCGTATTTAT'
3140 3150 GGGGAGTGCGGGACT.::::::::::::::::::::::::::::::::::::	3210 GGGGGTGGAGATGGA ::: ::::::: GGGAGATGGA	3280 TCGGTGGTATTTTA :::::::::::: TCAGTGGTATTTTA 2620	40 AGGAGGTGGGCATGC ::::::::::::::::::::::::::::::::::::	3410 ACTTATTGTGTCCCC :::::::::::::::::::::::::::::
M GGG H AGG	ж ж ж н	M TT H TT T	3340 M AG :: H AG	3 M AC :: H AC

lig. 3R

79	158	8 228	2 2 8 8 8 8	48 348	68	88 468	108 528
GTCGACCCACGCGTCCGCGGCGCGCGCGCGGGGGCCATCCAGACCCTGCGGAGAGCGAGGCCCGGAGCGTCGCC	GAGGTTTGAGGGCCCCGGAGACCGAGGGCCTGGCGGCCGAAGGAACCGCCCCAAGAAGAGCCCTCTGGCCCGGGGGCTGC	CHC	S TCT	R AGA	E GAG	K AAA	N AAC
		L CIA (A GCT	H CAT	R AGA	D GAT	ტ ტ
		V GTT (K AAG	I ATA	E GAA	E GAA	D GAT
		L CTG (P CCA	H H H C	L CTA	D GAT	S TCA
		L CIT (GGT	T T T	N AAC	V GTG	K AAA
		T ACG (R AGA	N AAC	G GGC	FIT	T C ACA A
		F TTT 2	A GCA	A GCA	PCCC	I ATT	TACC
			C TGC	E GAA	T ACT	E GAG	P CCA
		ACT 7	H CAT	E GAA	F TTC	R AGA	GGA
		CCAGZ	P CCT	K AAA	L	A GCC	K AAA
		3TTG(F	S TCA	EGAG	E GAA	A GCT
		M TTTGACAGTTGCCAGACT ATG	G GGG	T ACA	L CTG	E GAG	S TCA
		TLL	L CTG	F T T	D GAT	Y TAT	Y TAT
		TLL	TACC	V GTG	T T T	N AAT	E GAA
		CACAG	V GTT	E GAA	R AGA	C Tec	Q CAG
		3GGA(T ACA	E GAA	N AAT	L	F W TTT TGG
		36660	CCC	GGA	$rac{Y}{TAT}$	E GAA	F TTT
		GTGC	L CIG	A GCG	L	E GAA	A GCA
		TGGAACATGTGCGGGGGGACACAGTTTG	O CAA	H CAT	L	N AAT	I A 3 ATT GCA
GTC	GAGG	TGGA	S AGC	K AAG	R CGC	C TGC	TACG

Fig. 4A

H CAC

G GGG

E GAA

Y TAT

E GAG

R AGA

I ATT

V GTT

C

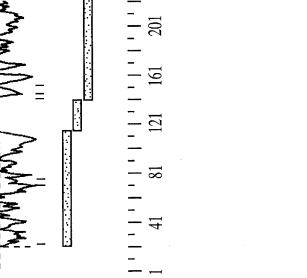
P CCA

E GAG

PCCT

1517 1596 1675 1754 2149 1359 1833 2070 1912 1991 2228 2307 GAAGAAGAAGACCACAAAAGACATGACTATCCAACTTTTTTATGACAAACTGCAAGGAATAAAGGAAGAATAAGTCCATG CATAGGTAGAATTAGTGAACTCTTTGGATCCTTTGTACAGATAAAGGTTATAGATTTTCTTGTGTTGAATATTAAAAAAG CAAGGATGTCTAACCATTAAGATTATCCAAAGTCAGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGA GGGATAGGTGGGCGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATGGCAAAAACCCCGTCTCTACAAAA TACTGTACCACAGAAGTTCTGTCTGCATCTTGGACCTGAACTTGATCATTATCAGCTTGATAAGAGACTTTTTGACTCT ATACAAAAGAAATTAGCCAGACATGATGGCGGGTGCCTCTAATCCCAGCTACTGGGGAGGCTGAGGTGGGAAATCGCT TGAACTCGGGAGGTGGAGGTTGTAGTGAGGCGAGATTGTGCCATTGCACTCCAACCTGGGCGACAGAGTGAGACTCCAT CTCAAAAAAAAAAAAAAAAAAAGATTATCCAAAAAGATATTGGACCTACTCTTTAGGATTTTTTTGGCGGGGGGT TAGAAATACTTCACAGAATTTGACATTTCAGTATAAATCTGTGACCTTAATATAATCACTTGGTTTTATATGTTAAATT GATTTGCAAGGGTTGTTATGCTATCAAATAAACAGACCTAAAATCTAGGAGACACTAGAACTTAATGAAGTTGCCCCTG TTACTGATTAGTAAATACTCCCATCTTCGTTGCAAAATTATCTCTGTATAACTACATATGATTATTTGAAATTTGT TAAACTTCATAAGTAATAGTTTGAGAATGTGGAAAAAGTAATTTGCTTTTCTGCTCTTAAAATATATTGATTAATGTT ACCAGAAAAAAAAAAAAAAAAGGGCGGCCGC

Fig. 4C



Cys out Tm ins

FIG 4D

60	160	208	256	304	352
GTCGACCCAC GCGTCCGCTG CGTTCTCACC CCTGGACCAC CCTGGGAGAA CAGTTGACCG AAGTTTGTTT GGCAGTTGCT GCTGGACT ATG TTT CTG CTT CTG GTG GTA CTC Met Phe Leu Leu Val Val Leu 1	CAG CTG CCC AGA CTT ACC CTC GCG GTT CCT CAT ACA AGA AGC CTA Gln Leu Pro Arg Leu Thr Leu Ala Val Pro His Thr Arg Ser Leu 10	AAT TCT GAA CAT GCC CCA GAA GGA GTC TTT GCA TCA AAA AAA GCA ASD ASD Ser Glu His Ala Pro Glu Gly Val Phe Ala Ser Lys Lys Ala 30	AGC ATC TTT ATG CAC CGT CGC CTC CTA TAC AAT AGA TTT GAT TTA 25. Ser Ile Phe Met His Arg Arg Leu Leu Tyr Asn Arg Phe Asp Leu 50	CTC TTC ACT CCC GGG AAC CTG GAG AGA GAG TGC TAT GAG GAG TTC Leu Phe Thr Pro Gly Asn Leu Glu Arg Glu Cys Tyr Glu Glu Phe 60 70	AGT TAT GAA GAA GCC AGA GAG ATC CTC GGG GAC AAC GAA GAA ATG Ser Tyr Glu Glu Ala Arg Glu Ile Leu Gly Asp Asn Glu Glu Met 75
GT(AA(AGC Ser	AAG Lys 25	GCA Ala	GAA Glu	TGT Cys

Fig. 4E

400	448	496	544	592	640
TCA Ser	TTA Leu 120	TAT Tyr	GCT Ala	ACC Thr	GGA Gly
AGA Arg	66C 61y	TAC Tyr 135	TCA Ser	AGA Arg	GCG Ala
ACA Thr	ACT Thr	GGT Gly	TCT Ser 150	TTC Phe	GAC Asp
ACC Thr	CTG Leu	CTT Leu	GGT Gly	ATT Ile 165	GAG Glu
CCA Pro 100	CTT Leu	TTA Leu	CAA Gln	ATC Ile	TCA Ser 180
GGA Gly	GGC G1y 115	GGC Gly	TAT Tyr	TCC Ser	TCC Ser
AAA Lys	ATG Met	TTT Phe 130	CCA Pro	CCG Pro	TCA Ser
GTC Val	GTT Val	GTT Val	CAG Gln 145	ACA Thr	TCG Ser
TCA Ser	GAT Asp	GTT Val	AGG Arg	CAC His 160	CCA Pro
TAT Tyr 95	ATT Ile	TTG Leu	AAT Asn	AGG Arg	TCT Ser 175
GAA Glu	AAA Lys 110	TTC Phe	TGT Cys	ACC Thr	TTG Leu
CGG Arg	GAG Glu	GTA Val 125	AAG Lys	AGG Arg	GTC Val
TGG Trp	AAA Lys	GGA Gly	ACC Thr 140	AGA Arg	GCT Ala
TTC	AAC Asn	GCT Ala	ATC Ile	ACA Thr 155	GAA Glu
ACA Thr 90	GTC Val	GCG Ala	TGT Cys	TAC Tyr	GAG Glu 170
ATC Ile	GAT Asp 105	ATT Ile	CTG	GTC Val	CAT His

Fig. 4F

8 8 9	736	783	8843 11110033 112033 11323 11323 11443 115043
CTA CCT TCC TAT GAA CAG GCA GTA GCT CTG ACC AGA AAA CAC AGT GTC	TCA CCA CCT CCA TAT CCT GGG CCA GCA AAA GGA TTT AGG GTA TTT	AAA AAG TCA ATG TCA CTC CCA TCT CAC TAAGCCCACC TTGCCGCCTT	GCTGTGGTCT GAATAATATG TTCTTCCTGA AACAACAACA ACAAAAAAT TTGCCTGTTC AGCTTTTTAT GACAAAGCAC AAGGAATAAA GGAACACTAT ATACAGAACA GAATTCACCA CAGCCCCGCT TTCAGCTCTG CCCCCAACTG GATTGCTGTC TGGTTCAACC TGCTTCCTCG AAGTTAAGAA GAAAGTGCCT TTTTGCAATG TAAACTGTAC TGGTTCAAAC ATTCTTGCTA CAGCTAGGTA CCTATAATCC CCACCTTCAG GAGACTTAGG CGGAGGGAT GAGAGTTCAA GGCCAGCCTG GGCCCTGTCA GGACGCTTCAG GAGACTTTGG AATAGAATAA TTAGAATTAA CAAACTAGA TTTTCAGTCT TAAGTCATGA TATTGGTAT ACTCTTCAGT AAGGTTTCTT TTTGGCTAGA AATACTTCAT AGAATTTGAC ACATCTTGCTG GGCCCTTGAT TTTTCTGTTTT AATTAGTGCA GAGGATTCAG CAAATTTGCA GGTCTTCATT TTGTTCCCTC GCTATCCATTG GAGGATTCAG CAAATTTGCA GGTCTTCATT TTGTTCCCTC GCTATCCATTG GAGGATTCAG CAAATTTGCA GCCAGGCGTG GTGCCCACA CCTGTGATCC AGAGGAGTCA AAGCAGAGAAAAC AAAGCAGAGA GAGAGAGAA ACAACCAGAG AAACCTTGTC TTGAAAAACA AAACAAAAAC AAAGAGAGAGA GAGAGAGA
Leu Pro Ser Tyr Glu Gln Ala Val Ala Leu Thr Arg Lys His Ser Val	Ser Pro Pro Pro Tyr Pro Gly Pro Ala Lys Gly Phe Arg Val Phe	Lys Lys Ser Met Ser Leu Pro Ser His	
185	210	220	

Fig. 4G

1623	1683	1743	1803	1863	1923	1983	2002
TTATGGGCCT	CATTACCCAC	ATCTTGAGAA	AGCCTCCAGA	TGGTCTTTAA	AGCCIGGICI	AAAAAAAAA	
SAGAAAAGAG ATGTCAAGAG GTTTTTTTTTTTTTTTT AAATTACTAT TTATGGGCCT	CACTIGGAAA AGIGCIIGCC AIGCAAAIAG AAGGACAGGA GIICAAICCI CAIIACCCAC	ATTTGAAACA AATAACAAGA AAAACAAACC AAAAAACCAA AACAAACAAA	GGCACTGTAA CTGAATCAGG AGCCTCCAGA	TCCAGGGAAA CGCTGTCTCA ACAAATAAAT AAATAAGTAA GTCAGTGAGG TGGTCTTTAA	ACCCAGCACT TGAGAGCCAA AGGCAGGCAG AGCTCAGTGA GTTGGAGACC AGCCTGGTCT	ACAAAGCAAG TICTAAGGGA GCCAGGGCAC AGAGAAACCC TGTCTGAAGG AAAAAAAAA	
TTTTTTTT	AAGGACAGGA	AAAAAACCAA	GGCACTGTAA	AAATAAGTAA	AGCTCAGTGA	AGAGAAACCC	
GTTTTTGTTT	ATGCAAATAG	AAAACAAACC	CTCAGGGCTA	ACAAATAAAT	AGGCAGGCAG	GCCAGGGCAC	
ATGTCAAGAG	AGTGCTTGCC	AATAACAAGA	CITGAGIGAA TACCGGIAAC CICAGGGCIA	CGCTGTCTCA	TGAGAGCCAA	TTCTAAGGGA	೧೯೭೦೮೯೦೯
GAGAAAAGAG	CACTTGGAAA	ATTTGAAACA	CTTGAGTGAA	TCCAGGGAAA	ACCCAGCACT	ACAAAGCAAG	AAAAAAAAG GGCGGCCGC

Fig. 4H

Ŋ	\vdash	ATGTTTCTGCTTCTGGTACTCAGCCAGCTGCCCAGACTTACCCTCGC 50
H	\leftarrow	
ტ	51	GGTTCCTCATACAAGAAGCCTAAAGAATTCTGAACATGCCCCAGAAG 97
田	51	
ტ	86	GAGTCTTTGCATCAAAAAAGCAGCAAGCATCTTTATGCACCGTCGCCTC 147
Ħ	101	
ტ	148	CTATACAATAGATTTTAGAACTCTTCACTCCCGGGAACCTGGAGAG 197
田	151	CTGTATAATAGATTTGATCTGGAGCTCTTCACTCCCGGCAACCTAGAAAG 200
ڻ ڻ	198	AGAGTGCTATGAGGAGTTCTGTAGTTATGAAGAAGCCAGAGAGATCCTCG 247
田	201	AGAGTGCAATGAAGAACTTTGCAATTATGAGGAAGCCAGAGAGATTTTTG 250

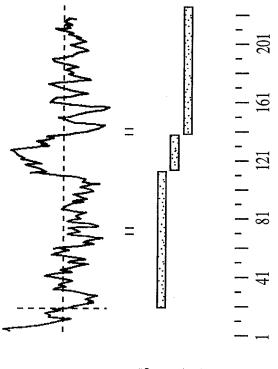
Fig. 41

GACAACGAAGAAATGATCACATTCTGGCGGGAATATTCAGTCAAAGGA 297	TGGATGAAGATAAAACGATTGCATTTTGGCAGGAATATTCAGCTAAAGGA 300	AACCACAAGATCAGATGTCAACAAAGAGAAATTGATGTTATGGGCCT 347	CCAACCACAAAATCAGATGGCAACAGAGAAAATAGATGTTATGGGCCT 350	TCTGACTGGCTTAATTGCGGCTGGAGTATTCTTGGTTGTTTTTGGCTTAC 397	GATTAATTGCTGCAGTATTTTTGGTTATTTTTGGATTAC 400	TGGTTACTATCTGTGTACCAAGTGTAATAGGCAGCCATATCAAGGT 447	TATCTTTGTATCACTAAGTGTAATAGGCTACAACATCCATGC 450			CGTCTATGAAAGGGGGAGGCACACTCCCTCCATCATTT 497
GGGACAACGAAGAAAT	TGGATGAAGATAAAAC	CCAACCACAAGATCAG	CCAACCACAAAATCAG	TCTGACTGGCTTAATT	TCTGACTGGATTAATT	TTGGTTACTATCTGTG	TIGGCTACTATCTTTG	ACHULACTULUS .		TCTTCAGCCGTCTATG
248	251	298	301	348	351	398	401	448	1	451
ტ	Ħ	Ŋ	田	ტ	耳	Ů	田	יי)	田

Fig. 4J

Fig. 4K

		200	Н
	SVSPPPYPGPAKGFRVFKKSMSLPSH 225	199	Ŋ
199		151	二
198	SSAVYTRRTRHTPSIIFRTHEEAVLSP.SSSSEDAGLPSYEQAVALTRKH	150	ტ
150		101	H
149	. PTTRSDVNKEKIDVMGLLTGLIAAGVFLVVFGLLGYYLCITKCNRQPYQG	100	Ŋ
100		51	田
66		50	ტ
50	. .	\leftarrow	田
49			ტ



Cys out Tm ins

FIG. 4M

				۷	19 /109		
79	152	26 212	46	332	86 392	106 452	126 512
ATA	H H H H	H CAC	C HGC	Y TAT	CII	O CAA	G GGA
TTAAAAAGAAAACCTTTACTGAATCAGCTGAGTGTTAATAATA	Q CAG	L CTC (N AAC	L CTG	S TCT (V GTT (P CCT (
TGLI	L TTA	L TTA	I ATT	T T T T	H CAT	T T T T	D GAT
CTGAG	G GGA	L TTA	Q CAA	V GTT	LCTT	A GCC	$_{ m L}$
rcągo	C TGT	L TTA	R AGA	T ACA	GGA	K AAA	R CGC
rgaa1	M ATG	L	ტ ტტტ	S AGT	T ACA	P CCA	K AAA
[TAC]	SGAT	Y TAT	T ACT	E GAA	L TTA	Y TAT	I ATC
ACCT	CAGAAAATCCAAGAACAGGGAT	C TGT	C H GC	PCCT	E GAA	V GTA	H H H C
3AAA?	AAGAA	T ACC	CIC	FTTT	S AGT	Y TAT	N AAT
AAAA	ATCC?	V GTT	Q CAG	N AAT	E GAA	L	N AAT
\mathtt{TTTA}	SAAAI	V GTT	C H H H H	K AAG	N AAT	I ATT	N AAT
AGAI	AACAG	L CIG	V GTT	PCCT	I ATA	N AAC	L CTA
CTT	CTG	년 년 년	S TCT	I ATT	Y TAT	S TCT	H H H T T
CGL	CTGA1	L	S TCG	S AGT	S TCT	N AAT	L CTA
AATGI	ATTC	R CGA	C TGT	S TCG	I ATA	D GAT	H T T T T
GGAZ	7005.	L CIA	G GGA	CTT	N AAT	L TIG	Y TAT
GTCC	TCT	C TGC	CTT	GGC	N AAT	Y TAT	L CTA
ACGC	CTTI	PCCT	I ATA	L TTA	GGG	LTG	H CAT
GTCGACCCACGCGTCCGGAAATGTCGTTCTT	CGAATTTCCTTGCCAATTCTGATCTG	$_{ m CTG}$	E GAA	N AAC	T ACT	A GCA	R AGG
GTCG	CGAZ	S TCT	K AAA	R CGT	L CIG	V GTA	L TTG

Fig. 5A

50/109

Fig. 5B

51/109

Fig. 5C

52/109

Fig. 5D

V P E N E A Q V I L F E H S A L * GTT CCT GAA AAT GAG GCA CAG GTC ATT CTT TTT GAA CAT TCT GCT TTA TAA CTCAACTAAATATTGTCTATAAGAAACTTCAGTGCCATGGACATGATTTAAAACTGAAAAAAAA
E A Q V I L F E H S A L * I GAG GCA CAG GTC ATT CTT TTT GAA CAT TCT GCT TTA TAA STCTATAAGAAACTTCAGTGCCATGGACATGATTTAAACTGAAACCTCCTTATATAATTATAC TAATGAATTATATGGGTTAGCATTATTAAAATATGTTTTTAAAAAAAA
V P E N GTT CCT GAA AA' CTCAACTAAATATTO TTTAGTTGGAAATA' GCGGCCGC

Fig. SE

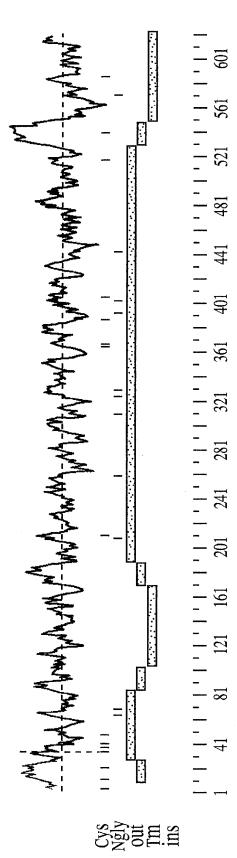


FIG. 5F

•	
120 200 SFNHMPKLRTF :	230 240 250 260 270 SDWLRQRPRVGLYTQCMGPSHLRGHNVAEVQKREFVCSGHQSFMAPSCSVLHCP :::VGMVA
110 190 NNNITRLSVA : : :	260 EFVCSGHQSFI
180 LRDLEVLTLN: : :.:. LVSVQYLNLQ: 160	250 GHNVAEVQKR: :: VA
170 SCIEDGAFRA STEPRGVFND 150	240 TQCMGPSHLR
160 160 KNLQLDYNQI ::::::::::::::::::::::::::::::::::::	230 LRQRPRVGLY ::. VGM-
80 150 PRKAFRGAVDI :::.:.	210 220 RLHSNNLYCDCHLAWLSDW
	210 Slit RLHSNNLY 325
	140 150 160 170 180 190 180 180 180 SENQIQAIPRKAFRGAVDIKNLQLDYNQISCIEDGAFRALRDLEVLTLNNNNITRLSVASFNH ::::::::::::::::::::::::::::::::::::

Fig. 5C

290 340 310 320 330 340 CRGKGLTEIPTNLPETITEIRLEQNTIKVIPPGAFSPYKKLRRIDLSNNQISELAPDAF	:::::::::-:	360 370 380 400 410 YGNKITELPKSLFEGLFSLQLLLLNANKINCLRVDAFQDLHNLNLLSLYDNKLQTIAKG :::::::::::::::::::::::::::::::::	430 440 450 460 470 480 HLAQNPFICDCHLKWLADYLHTNPIETSGARCTSPRRLANKRIGQIKSKKFRCSAKEQY :::: 210	500 510 520 530 540 550 LSGDCFADLACPEKCRCEGTTVDCSNQKLNKIPEHIPQYTAELRLNNNEFTVLEATGIF .:.:.::::::::::::::::::::::::::::::::
280 290 Slit AACTCSNNIVDCRGKG	325	350 360 Slit QGLRSLNSLVLYGNKI :: 325LRI	420 430 Slit TFSPLRAIQTMHLAQN 325	490 500 Slit FIPGTEDYRSKLSGDC 325

Fig. 5H

560 570 580 590 600 610 620 KKLPQLRKINFSNNKITDIEEGAFEGASGVNEILLTSNRLENVQHKMFKGLESLKTLMLRSNRITCVGND ::::::::::::::::::::::::::::::::::::		630 640 650 670 680 690 SFIGLSSVRLLSLYDNQITTVAPGAFDTLHSLSTLNLLANPFNCNCYLAWLGEWLRKKRIVTGNPRCQKP ::::::.:: GFSGINNLKHLILSHND	0 720 730 740 750 760 FTCDDGNDDNSCSPLSRCPTECTCLDTVVRCSNKGLKVLPKGIPRDVTELYLDGN :	770 780 800 810 820 830 QFTLVPKELSNYKHLTLIDLSNNRISTLSNQSFSNM-TQLLTLILSYNRLRCIPPRTFDGLKSLRLLSLH ::::::::::::::::::::::::::::::::::
560 570 580 KKLPQLRKINFSNNKITDIEEGAFEG. :::::	LRRLSLSHNPIEAIQPFA- 230 240		700 71 YFLKEIPIQDVAIQD	
Slit	325	Slit 325	Slit 325	Slit 325

Fig. 5

900 DKILLTTPSK	 	970 NPCKHGGTCH : .:: -PSMRG	1040 EEKLDFCAQD	0 1070 1080 1090 1100 1110 FKCDCTPGYVGEHCDIDFDDCQDNKCKNGAHCTDAVNGYTCICPEGYSGLFCEF ::
0 860 870 880 890 900 ALSHLAIGANPLYCDCNMQWLSDWVKSEYKEPGIARCAGPGEMADKLLLTTPSK		960 DCDVPIHACIS ::: -CQNP	0 1000 1010 1020 1030 1040 FEGENCEVNVDDCEDNDCENNSTCVDGINNYTCLCPPEYTGELCEEKLDFCAQD :::	1100 TDAVNGYTCICP :: TSSIN
880 VKSEYKEPGI	. : LAS	950 TCPYGFKGQL	1020 VDGINNYTCI : V	1090 KCKNGAHCTI :TS
870 DCNMQWLSDW	NCKLLGLRDW 370	940 NSDPVDFYRC :	1010 DNDCENNSTCV: : .::	1080 DIDFDDCQDN
860 AIGANPLYCI	SLIHLQANSNPWECNCKLLGLRDWLAS-0360370	930 SNPCKNDGTCI	1000 NCEVNVDDCE1	1070 CTPGYVGEHC
850 FNDLSALSHI	::::: SSLIHI 350	920 IILAKCNPCLS : II	990 :::	
840 85 GNDISVVPEGAFNDLS		910 920 930 940 950 960 970 KFTCQGPVDVNILAKCNPCLSNPCKNDGTCNSDPVDFYRCTCPYGFKGQDCDVPIHACISNPCKHGGTCH :::::::::::::::::::::::::::::::::	980 LKEGEEDGFWCICADG :	1050 106 LNPCQHDSKCILTPKG
Slit (325 .	Slit 1 325 ·	325	Slit 325

Fig. 5J

1180 PSAKVRPQTN	:: AWHKV	1250 ELLALDQSLS : :. AVLPVQIQLT 0	1320 NSELQDFQKV : .:. QEVEKL 520	1390 ICLPINAFSY :
1120 1130 1140 1150 1160 1170 1180 SPPMVLPRTSPCDNFDCQNGAQCIVRINEPICQCLPGYQGEKCEKLVSVNFINKESYLQIPSAKVRPQTN	: : : :	1190 1200 1250 1250 1250 1250 1250 1250 125	1260 1270 1280 1290 1300 1310 1320 LSVDGGNPKIITNLSKQSTLNFDSPLYVGGMPGKSNVASLRQAPGQNGTSFHGCIRNLYINSELQDFQKV :: ::::::::::::::::::::::::::::::::::	1330 1340 1350 1360 1370 1380 1390 PMQTGILPGCEPCHKKVCAHGTCQPSSQAGFTCECQEGWMGPLCDQRTNDPCLGNKCVHGTCLPINAFSY ::: NEAFDILLAFFFIL
1160 GEKCEKLVSVI	: SPI 420	1230 :SHPASAIYSVE' ::	1300 LRQAPGQNGT:	1370 MGPLCDQRTNI
1150 PICQCLPGYÇ		0 1220 LYRGRVRASYDTG : .: -FWERIPTS	1290 VGGMPGKSNVAS .:.: SMSGKTSLI-	1360 AGFTCECQEGW :
1140 IGAQCIVRINE	·:· VVK	1210 KGDKDHIAVELYRG	1280 :: : : :	1350 AHGTCQPSSQA
1130 SPCDNFDCQN		1200 DSGILLYKGI :	1270 128 IITNLSKQSTLNFDSPL .::::::	1340 CEPCHKKVC?
			0	
Slit	325	Slit 325	Slit 325 49	Slit 325

Fig. 5K

Fig. 5L

70 FATT		140 3GGT	 	210 3CGC		280 ACCGC ::: ACC
TAT)525,		GATC		GCAC :: AC
0 TCCA		0 CACT] 	0 GAAA		0 GGTG
60 FTGTT		130 CAGAC		200		270 ACAAG
GCC	 	CCTC)550;		TGA?
50 TACI	[]]	120 .crese	 	190 GGAGG	 	260 GATCC
BCTC	 	1 3CAC	 	1 3AAG		2 3GCG
TGG	i !	3000	i !	GAG	i i	GCT
40 TGAG	 	80 90 100 110 120 140 TTGTGCACATTTTCCCTGGCACTCTGGGTTGCTAGCCCCGGGGCACTGGGGCCTCAGACACTGCGCGGT		150 160 170 180 190 200 210 TCCCTCGGAGCAGCAAGCTAAAGAAAGCCCCCCCAGTGCCGGCGGGGGGAAAGATGCGC	 	220 230 240 250 260 270 280 GGCGTTGGCTGGCAGTCCCTGTCCCTGTCCTGAACAAGGTGGCACCGC ::: :: ::
TGCC	 	AGCC	 	GTGC	 	19999
) CGTG) IGCT	[CCCA	1 1 1	CTG
30 SAGGC	į	100 3GGTT		170 16CCC	! ! !	240 GTCG:
TGGG	 	TCTO		GAAZ		CCCI
20 GCGG	 	90 GCAC	 	160 CTAAA	 	230 GCTGT
BAGG	 	CTG		1 1AGC'	1	2 3ATG
GGA	!	TTC		AGC.	1	GCAC
10 GGG1	 	80 .CATT		150 GAGC	 	220 GCTG
AGCA	 	IGCA	 	SICG	 	9 I H H !
CAG.	i	TTG	 	TCC	 	999
10 20 40 50 70 Slit cagagcaggagggggggggggggggggggggggggggg	325	Slit	325	Slit	325	Slit 325
01		01		01		01

Fig. 5M-1

350	:::	420 3AAG	490 3AAA	560 11CC
GCAG	! ! 	TACO	ATTG .::. ITTA	560 TGTTTCC ::::
TGC	 	AAT'	ACCAT: .:	AGC
340 3CGC	 	410 CAAG	480 LAGC	550 CTTC
CTG	i	TCA(GAT	TCAC(.:. ACG
o ceee	5 C C C	2 AACA 	0 ATAA :.:: AAAA	0 AAATCA :::. AATACG 80
330	- CACG	400 AATA 	470 'AGAA' : • • • :	540 CAGA :
ACTG	 	IGGA	470 ATGGAGAATA : TAAAAGAAA 40	540 TTAAACAGAAATCAC ::::: TTAATAATACG- 80
O TGG	i i	00 'AAA'	460 470 TCTTCAGCTTATGGAGAATAA ::::::::::::::::::::::::::	10 10 10 10 10 10 10 10 10 10 10 10 10 1
320 ACAGT	 	390 ATTTA 	460 TCAGC' :::: TCAGA'	530 CTGCG
AGC] 	TGG I	::::::::::::::::::::::::::::::::::::::	3AGA .: 3TG-
300 340 320 330 340 350 340 350 340 350	! ! !	370 380 400 410 420 CGCAACACGAGAGATTTAAATGGAAATAACATCACAAGAATTACGAAG	440 450 460 470 480 490 TTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAA ::::::::::::::::::::::::::::::::	510 520 530 540 550 560 TCTTAAAGAACTAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCC ::::::::::::::::::::::::::::::
3 CTC	! !	3 3GAG	4 TAA	AACT:
CTTG	f 	CACC	CATC	AAG <i>P</i> : <i>P</i>
300 TGCT	[]	370 :GCAA:	440 TAGA	510 CTTA : C
CAGI	; ; !		TCTT	
3606	1 ! !	ATCC 3TC-	7. TGG	CCAGGA :.:.: -CTGAA
290 CCC	! ! !	360 CCCAGGAATATCC :::::::: -CCGGAAATGTC- 20	430 TTGC	500 ATT(
GTG		2AGG	3ATT	3AGC
AGGC	 	360 GCCCAGGAATATCCCC ::.::::-:: CCGGAAATGTC	430 ACAGATTTTGCTGGTC	500 GAGGAGCATTCCAGGA :.:.: CTGAA
290 Slit AGGCGTGCCCGGCGCA	325	Slit 325	Slit 325	Slit 325
S		Ø	ω	ω

Fig. 5M-2

630 CAATC		700 CTGTA ::. GTT 150	770 ACTAG	840 TGTAT :: AT 200
620 ccaaattcagg 	ccaagaacagg 130	690 AACCAGATCAG : A	760 ATAACAACATT : A	830 ITCAAACAACC
610 CTCAGTGAAAAC	-ACAGA-AAATCCAAGAACAGG 120	680 AACTGGATTACAA :::::::: TGGATTACA- 140	750 CACTCTCAACAA' ::::: CTACGA	820 TTTCGACTGCA: ::: TTT
600 CAGGCTTGATC		670 AAAAATTTGC <i>?</i> .:.::: -GATATGTG	740 TGGAAGTGCTC : :: TTGC	810 ACTTAGGACTTTT .::::
590 CGAAGCTATA	ccaarrcrgarcrga- 100	660 AGTTGACATA	730 :::: ::: CTCTGCCT-	800 CATATGCCTAA : . : . : . CTGTTA
580 CTTGGGACTG		650 TCCGTGGGGC	720 ATTCAGGGCT::	780 790 81 CTGTGGCAAGTTTCAACCATATG :::: .::: .:::: CTGTTTCTGGTTGTTACCTGTTA 180 190
		640 650 700 700 700 680 690 700 CCAAGGAAAAGCTTTCCGTGGGCCAGTTGACATTAAAAAATTTGCAACTGGATTACAACCAGATCAGCTGTA .::::::::::::::::::::::::::::::::::::	710 720 740 750 760 770 Slit TTGAAGATGGGGCTCTCCGGGACCTGGAAGTGCTCACTCTCAACAATAACAACATTACTAG :: ::::::::::::::::::::::::::::::::::	780 830 840 ACTTTCTGTGCCAAGTTTCAACCATATGCCTAAACTTAGGACTTTTCGACTGCATTCAAACAACCTGTAT ::::::::::::::::::::::::::::::::::
Slit	325	Slit 325	Slit 325	Slit 325

Fig. 5M-3

910 TCAGT :: .: TCT	980 GTGG	1050 .CAAT	1120 ATAC .:.:
900 TTGGTCTGTACACI ::::::::::::::::::::::::::::::::::	970 980 AGAATTTGTCTGCAGTGG ::::::::::::::::::::::::::::::::::	1040 TGTACCTGTAGCAA ::: :: .:: -GTAACTTAGGC	1070 1080 1090 1100 1110 1120 GGGAAAGGTCTCACTGAGATCCCCACAAATCTTCCAGAGACCATCACAGAAATAC : :::::::::::::::::::::::::::::::::::
890 36CCTCGGG 3.	960 CAAAAACG	1030 CTGCCGCC	1100 ATCTTCCAGAGA ::::::::::::::::::::::::::::::::
880 TCGCCAAAGGCC ::::: AAATAC- 220	950 AGCCGAGGTT :: AGC	1020 TGCACTGCC:::::	1090 CCCCACAA?
870 TCCGACTGGCT	940 GCCATAATGTA :	1010 TTGTAGTGTTT	1080 CTCACTGAGAT : :::: 'CCTAAGA-
860 GGCCTGGCTC .: AG	930 CACCTGAGAG	1000 TGGCTCCTTC	1070 TGGGAAAGGTC .: :: AGTATTC
850 860 910 IGTGACTGCCACCTGGCTCTCCGACTGGCTTCGCCAAAGGCCTCGGGTTGGTCTGTACACTCAGT ::::::::::::::::::::::::::::::::::::	920 930 940 950 960 970 980 GTATGGGCCCCTCCCACCTGAGAGGCCATAATGTAGCCGAGGTTCAAAAACGAGAATTTGTCTGCAGTGG :::: :: :: ::::::::::::::::::::::::	990 1000 1010 1020 1030 1040 1050 TCACCAGTCATTTATGGCTCCTTGTAGTGTTTTGCACTGCCCTGCCGCCTGTACCTGTAGCAACAAT ::::::::::::::::::::::::::::::::	1060 ATCGTAGACTGTCGT ::::. CTTTCGA(
Slit 325	Slit 325	Slit 325	slit 325

Fig. 5M-4

1190 AGACGAAT	:. ::: AAAGT-GAAT 370	1260 TGAATTCA ::::	1330 CTTACAGC ::::: CTAACA 420	0 1400 CACAACTTGAA :::::::-
1180 AAAAAGCTT	::::::::::::::::::::::::::::::::::::::	1250 TACGCTCTC :::	1320 13 ACTGTTTTCCTTACA :.:::::: TAATTCTAACA 410 420	1390 GATCTCCACA : :: GCA
1140 1150 1160 1170 1180 1190 CAATCAAAGTCATCCTCGGAGCTTTCTCACCATATAAAAAGCTTAGACGAAT	TATAT 350	1210 1250 1260 TCAGATCTCTGAACTTGCACCAGATGCTTTCCAAGGACTACGCTCTCTGAATTCA :::::: ::::::::::::::::::::::::::::::	1280 1290 1300 1310 1320 1330 AATAAAATCACAGAACTCCCCAAAAGTTTATTTGAAGGACTGTTTTCCTTACAGC ::::::::::::::::::::::::::::::::::	1350 1360 1370 1380 1390 1400 CCAACAAGATAAACTGCCTTCGGGTAGATGCTTTTCAGGATCTCCACAACTTGAA::::::::::
1160 CTGGAGCTTT	::::. : CTGGGAATAA 340	1230 :ACCAGATGCI	1300 CCCCAAAAGTI : : ATTG	0 1370 TGCCTTCGGGTAG? ::::: : -GCCTTTG
1150 GTCATCCCTC		1220 CTGAACTTGC	1290 ::: AGC	1360 SATAAACTGCC :::
1140 CACAATCAAA		1210 AATCAGATC1	1280 3AAATAAAA1 	1350 IGCCAACAAC : ::: : I-CCAAAA
1130 Slit GTTTGGAACAGAACA	:::::: 325TGTATCTGA 330	1200 Slit TGACCTGAGCAATAA :.:: 325 TAAC	1270 Slit CTTGTCCTCTATGGA :::: 325 CTTGT	1340 Slit TCCTATTATTGAATG : ::.: :.:: TTCTGTATGTATAT- 430

Fig. 5M-5

1470 GCCATT :	1540 GATTATCTCC:::: -TAAATCTTC 530	1610 AAAGAATTGG :.::: ATTTATATTT 550	1680 GATTAT
1460 :: :: :CA	1530 GGCTAGCGGATTAT :::: .::: GACTTTTAAAT 530	1600 GCAAACAAAAG. :	1670 CAGGTACAGAA
1450 GGGACCTTTTCA ::::: 1TTCA 490	1520 15 CATCTCAAGTGGCTAG ::::::	1590 CCCGCCGCCTG	1660 AGTATTTCATTC ::::::: AGTATTTAAT 590
1440 ccarcgccaa(1510 TTGTGACTGC(::	1580 TGCACCAGCC	1640 1650 1660 TCCGTTGTTCAGCTAAAGAACAGTATTTCAT::::::::::
1430 AGCTTCAGA	1500 CCCCTTTATTT .:::::	1570 GGTGCCCGT	1640 GTTGTTCAG::::: TTTGTTC:
1420 FATGACAACA ::::::: AATAATAA	1490 IGGCCCAGAA .:.::::	1560 rgagaccagr	1630 AAGAAATTCCG : . : . : : AGGTATCTT
1410 1420 1430 1440 1450 1460 1470 CCTTCTCTCTCTCTCTAACAAGCTTCAGACCATCGCCAAGGGGACCTTTTCACCTCTTCGGGCCATT ::::::::::::::::::::::::::::::::::	1480 1530 1540 CAAACTATGCATTTGGCCCAGAACCCCTTTATTTGTGACTGCCATCTCAAGTGGCTAGCGGATTATCTCC ::::::::::::::::::::::::::::::	1550 1560 1570 1580 1590 1600 1610 ATACCAACCGATTGAGACCAGTGCCCGTTGCACCAGCCCCGCCGCCTGGCAAAAAAATTGG ::: GTAATTTATATTT 550	1620 1630 1640 1650 1660 1670 1680 ACAGATCAAAAGAAATTCCGTTGTTCAGCTAAAGAACAGTATTTCATTCCAGGTACAGAAGATTAT :::: ::: ::: ::: :::::::::::::::::
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 5M-6

1760 CAGTAGATTGO :. TAO TCTCAATAATA 	CGATCAAATTAAGTGGAGACTGC ::::::: -GATCTAGTTT 600 CAGTAGTTT	1780 1780 1780 1780 1780 1780 1850 1850 1850 1920 1920 1920	1790 CCCGGAGCA(::	TTAAGAAGG	1810 1810 ::::: CACTGCAGA(::::: 640 1880 TTCCTCAATTA(::::: TACCT 660 1950 AGCATCTGGTG
1770 1780 1790 1800 CTCTAATCAAAAGCTCAACAAATCCCGGAGCACTTCCCCCAGTAC :::::::::::::::::::::::::::::::::::	GGAGACTGCTTTGCGGATCTGGCTTGCCCTGAAAAGTGTCGCTGTGAAGGAACCA ::::: 610 1770 1780 1880 1890 1890 1800	1790 1800 1810 1790 1800 1810 CCCGGAGCACATTCCCCAGTACACTGCAGA(::::::::::::::::::::::::::::::::::	1800 1810 CATTCCCCAGTACACGCAGA :::::::::::::::::::::::::::::	1810 1810 :::: CACTGCAGA(::::: 640 1880 TTCCTCAATTA(:::: FACCT 660 1950 AGCATCTGGTGT CTTCGG	

Fig. 5M-7

0	∢ ∢	O Ü 1	0 H	0 H • H
2030	CTCA.	2100 CTGTG	217(ITCT:	2240 rggcr
	4AGC(4GTT(rcca:	4GAG.
2020	rggai	2090 GACTC?	2160 TACTC1	2230 TTGGGA::::
2	3GAT	2(IAGG <u>i</u> 3	2: IGATA	22 IGGTT :: :: IGTTT 760
0	CAAG(D TTCA: .:::	CATT	0 2230 GGCTTGGTTGGGAG :::::::::
2010	IGTT(2080 CAGTT	2150 3GGGC	2220 ACCTG
	AAGA!	ATGA(::	ACCA(IGCT;
2000	AAATACTTCTTACGAGTAATCGTTTGGAAAATGTGCAGCATAAGATGTTCAAGGGATTGGAAAGCCTCAA :::::::::::::::::::::::::::::::::	2050 2060 2070 2080 2090 2100 AGCAATCGAATAACCTGTGTGGGGAATGACAGTTTCATAGGACTCAGTTCTGTG :::::::::::::::::::::::::::::::	2110 2120 2140 2150 2170 CGTTTGCTTTCTTTGATAATTACTACAGTTGCACCAGGGGCATTTGATACTCTCCATTCTT :::::GCTTTC	2180 2230 2240 2240 2240 2220 2230 2230 2240 TATCTACTCTAAACCTCTTGGCCAATCCTTTTAACTGTAACTGCTACCTGGCTTGGTTGG
2	TGCA	TGTG:	ACAG	2 ACTG
0	AATG	0 CCTG': .: .CA'	O TACT	0 TTTA : T
1990	GGAA	2060 AATAAC ::::: AATAAC	2130 AAATT	2190 2200 CCTTGGCCAATCCTT:::::::::::::::::::::::::
	E I I I I I I I I I I I I I I I I I I I	TCGA:	AATC	CCAA :: AA
1980	TAATC :.:: TTATC	2050 AGCAA	2120 ATGAT	2190 :CTTGG :::::
, 	ACGAGT::::	2 3AGAP	Z A T D T :	2 CCTC::::ACATC
7.0	CTTACG. :	10 FGTTG	10 FTCTT :::	30 CTAAACCT :::: AACÄT
1970	TACTIC ::::: TACTI-	2040 ITGATG	2110 TTGCTTT(:::: GCTTT(730	2180 FACTCTZ
	AAATACTT :::::: ATACTT	AACTT:::AAC700	3GTT1	ratci
	Slit 7 325 -	2040 Slit AACTTTGATGTTGAGA ::: 325 AAC700	slit (325 -	Slit 3
	Ω,	ω · ·	Ø	o

Fig. 5M-8

2310		2380 TCTC::::::::::::::::::::::::::::::::::	2440 2450 TTTGAAGGTCTTGCC:::::::::::::::::::::::::	2520 GGAA
200) 	2 TTT : :	D H	2 AAG
)TAC	TTA(238 CCACTITCT ::::::: -CTTTGTCT 840	3GT(::.	
0 7 A A 2	:::::: -GAAGTAC 810	0 2	10 ::: \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	0. 1. 1. 1. 1. 1.
2300 AAGA		2370 CTCC	2440 24. TTTGAAGGTCTTG ::::::::::::::::::::::::::::::::	2510 TGGT
T T		B I I	GGT	CAC
2260 2270 2280 2290 2300 2310 2310 2310)) 1	2330 2340 2350 2360 2370 2380 CAGGACTTCACTTGTGATGACGAAATGATGACAATAGTTGCTCCCCACTTTCTC :::::::::::::::::::::::::	2400 2410 2420 2430 2440 2450 GTACTTGCTTGGATACAGTCGTCCGATGTAGCAACAAGGGTTTGAAGGTCTTGCC ::::::::::::::::::::::::::::::	TTA
2290 TACT	· 	2360 ATGATGACAA' .::.:: -AGAAGACTT' 830	2430 CAAC	2500 CAAT
2. ATA	• 1	2. TGA(.:: AGA(830	2 4GC, C,	AAACC:
) \ \ \	TGCCTT	2360 IGATGACAA ::::::: AGAAGACTT 830	ATGT7	2 GAAACC :::: -ATACC
30 4 A A 4		50 VAA:	410 2420 ATACAGTCGTCCGATG' ::::::::::::::::::::::::::::::::::::	30 ATG(
2280	.:::: ATCAAA 80	2350 GGAA	2420 3TCCG3 .: CCT'	2490 TCTGGATG::::::
ΔTC		GAC) 	TCT(
\d \d \L		GAT	10 TACAG ::::: TACAG	GTA
2270 ATCC	A	2340 TTGT	2410 GATA(::: ATA(2480 AGTT
2 4	: *******************************	ACT	1 dg 1	2 AGA
ָרָ: יין	AAA.		GCTT(.:. .GCA 860	CAC
50 70 70	-ACZ	2330 AGGAC: :.: AAGTC: 820	00 TT7 	70 rGT(
2260	, ₹	2330 CAGGACTT: ::::: AAAGTCTT 820	2400 STACT	2470 AGATG'
Δ.	ATT7	ATTC ·:· TTAZ	.A—-	AAG2
מטע	TAZ	CC.	:TG2	CC
2250	.:. TAA	2320 GTGG	2390 CTAC	2460 TATT
2	.:: AAG	2 ATG	23 TGTCC: ::: AATCC: 850	2 GGT
	######################################	2320 CAGGATGTGGCCATT .:.	2390 GCTGTCCTACTGAAT:::: ::: ATAATCCTATTGAA- 850	AAA : A
	TI 6			t GA .: 5 AA
2250 2250 + 1 1 2 2 3 3 4 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4 5 4	325	Slit 325	Slit 325	2460 2470 2480 25500 2510 2520 Slit GAAAGGTATTCCAAGAGTTGTATCTGGATGGAAACCAATTTACACTGGTTCCCAAGGAA ::::::::::::::::::::::::::::::
Ü	4	U 2		- -

Fig. 5M-9

2590 AATCAGA	: ::.: :. TTTAGTGG 950	2660 CTCCTCG	2730 GCCTGAA .::::: ACCTTAA 1050	90 2800 ACTGTGATTGTA : :::. GATAATGAT
2580 ACGCTTTCT	: : TTTT	2650 AGATGTATTC ::: TAATGA	2720 27 ITCTGTTGTGCCTG: :::::::::::::::::::::::::	2790 CTTTACTGT :: GA
2570 ACAGAATAAGC	::::::::::::::::::::::::::::::::::::::	2640 265 CAACCGTCTGAGATGT ::::::. GTCA-TAATGA 990	2710 2720 2730 CATGGAAATGACATTTCTGTTGTGCCTGAA :::::::::::::::::::::::::::::::::::	2780 SAGCCAACCCT
2560 TTAAGTAACA	::	20 2630 CTTAATTCTTAGTTAC :::::. ATTTGATCTTAA	2700 ACTITCTCTACATGG; :::::::: ACATTCAGTTTGT; 1020	2770 CTAGCAATTG(::::: -TAGCATT
2550 ACTTATAGAC	:: TTAGGA 930	2620 2630 CTCACCTTAATTCTTAG :::::::	2690 2700 TTCGATTACTTTCTCTA	2760 CATTATCACAT :::: AATAAT
2540 ACATTTAAC	.:: TCAAGAA	2610 sacccagcrc : \A	2680 TTAAAGTCTC ::::: TTAAAT	2750 2 ATCTTTCTGCATTA : ::: AAACAGAATAA 1070
2530 2540 2550 2560 2570 2590 2590 CTCTCCAACTACAACTTTAACATTAGACTTTAAGACTTAAGACTTAAAGAAAAAAAA	:::::: TCCTGAAAATTCAAGAA- 910 920	2600 2650 2660 GCTTCAGCAACATGACCCAGCTCCTCACCTTAATTCTTAGTTACAACCGTCTGAGATGTATTCCTCCTCG ::::::::::::::::::::::::::::	2670 2720 2730 2730 2730 2720 2730 2730 27	2740 2750 2760 2770 2780 2790 2800 GGTGCTTTCAATGATCTTTTTTTTATCACATCTTAGCAACCCTCTTTACTGTGATTGTA : :::::::::::::::::::::::::::::::::::
Slit	325	Slit 325	Slit 325	Slit 325

Fig. 5M-10

2810 2820 2830 ACATGCAGTGGTTATCCGACTGGGTGAAT	:::: ACATTTGAAAATA' 90	2880 2890 2900 TGGAGAAATGGCAGATAAACTTTTACTCACAACTCC :	2950 2960 2970 2980 GTCAATATTCTAGCTAAGTGTAACCCCTGCCTATCAAATCCGTGT : :::::::::::::::::::::::::::::::::	3020 3040 ATCCAGTTGACTTTTACCGATGCACCTGTCCATATG :::: :::::::::::::::::::::::::::::::
2820 2830 2840 2850 2860 2870 CCGACTGGGTGAATATAAGGAGCCTGGAATTGCTCGTTGTGCTGGTCC	.::::: TGGGAGCAT 1110	2890 2930 2940 TAAACTTTTACTCACAACTCCCTCCAAAAATTTACCTGTCAAGGTCCTGTGGAT :::::::	2960 3000 3010 AAGTGTAACCCCTGCCTATCAAATCCGTGTAAAAATGATGGCACATGTAATAGTG ::::::::::::::::::::::::::::	3030 3040 3050 3060 3070 ACCGATGCACCTGTCCATATGGTTTCAAGGGGCCAGGACTGTGATGTC :::: ::::::::::::::::::::::::::::::::
0 2870 TGTGCTGGTCC	: :::. :::: -CTTTGAAGATCC 1120	0 2940 GTCCTGTGGAT	0 3010 ATGTAATAGTG :	0 3080 GTCCCAATTCA :::: ATTCA

Fig. 5M-11

3150 TGGATTC :: :.: TGCAAAC 1230	3220 GATAATG :	3290 AGTATAC	3360 TTCAAAG
3140 3150 AGGAGAAGAAGATGGATTC :::::::::::-::	3210 IGATTGTGAA	3280 rgcccaccrg : : rac	3350 3CCAGCACGA
3130 AAAGGA	3170 3180 3190 3200 3210 3220 GATGGATTTGAAGGAAAATTGTGAAGTCAACGTTGATGATGTGAAGATAATG : :	3240 3250 3260 3270 3280 3290 CTACATGTGTCGATGATTAATAACTACACATGCCTTTGCCCACCTGAGTATAC .: :::::::::::::::::::::::::::::::::::	3310 3320 3330 3340 3350 3360 GGAGAAGCTGGACTTCTGTGCCCAGGACCTGAACCCCTGCCAGCACGATTCAAAG ::::::::::::::::::::::::::::::::::
3120 ACTTGCCACTT:::::-:::	3190 ATTGTGAAG1 	3260 TAATAACTACAC :::: CTTCA-	3330 GCCCAGGACC ::: TGTC?
3110 ACATGGAGGA	3180 3AAGGAGAAA	3250 CCGATGGCAT' :.::: TAGCAT' 1260	3320 GCTGGACTTCTGTG ::.::::::: TCTAAACATCTATT 1280
3100 .cccargraaz 	3170 GATGGATTT(3240 CTACATGTG: .:	3310 GGAGAAGCTG::
3090 TGCCTGCATCAGTAA : :::: TCTTCAGG	3160 TGGTGTATTTGTGCT::::: TTTTGGGC	3230 ACTGTGAAAATAATT :::: ACTG	3300 AGGTGAGTTGTGTGA
Slit TGCC : 325 T	Slit TGGT : 325 T	Slit ACTG' ::: 325 ACTG- 1250	Slit AGGT 325
O2	01		e superior de la companya de la comp

Fig. 5M-12

3430 GACATCG	3500 GCTATAC ::: ATAA 1360	3570 :CTCGTACC :.:::	0 3640 GCCAATATGTC ::::::: CAA-ATGGC
3420 GAACACTGC	3490 SCAGTGAACG	3560 ATGGTCCTCCCT(::::::: ATATTCATCACA)	3630 AAATGAGCCA :: CA
3410 AGGTACGTAGGT ::::: TTACGTT 1320	0 CCCACTGCACAGATG : :: :: -CATCTTCA	3540 3550 3560 357 TGAGTTTTCTCCACCCATGGTCCTCCCTCGTAC :::::::::::::::::::::::::::::::::	3590 3600 3610 3620 3630 3640 TTGATTGTCAGAATGGAGCTCAGTGTATCGTCAGAATAAATGAGCCAATATGTC :::::::::::::::::::::::::::::::::::
90 3400 GTGACTGCACACCAGGG' ::::::: GTGGCAGAGCAT' 1320	3470 ACGGAGCCCACT :::	3540 CTGTGAGTTT :	3610 3620 GAGCTCAGTGTATCGTCAG.::.::.:.:.:.:.::::
3390 CAAATGTGAC ::::: GTGGC	3460 CAAGTGTAAAA ::::: ATTGTGTTA	3530 ACAGTGGCTTGTT ::::::: -CTTGGGCT-GTT 1380	3600 TCAGAATGGA :.: :CCTG
3380 CAAAGGGATT	3450 3460 CCAAGACAACAAGTGTAA. : ::: .::::-:	0 CCCCGAAGGTTACA ::.:: CCAGAGCT	3590 36 ATTTTGATTGTCAGA :: :: :: ATGATGGCCTG- 1430
3370 3380 3410 3420 3430 Slit TGCATCCTAACTCCAAAGGGATTCAAATGTGACTGCACACCAGGGTACGTAGGTGAACACTGCGACATCG ::::::::::::::::::::::::::::::::::::	3440 3450 3460 3470 3480 3490 3500 ATTITGACGACTGCCAAGACAACAAGTGTAAAAACGGAGCCCACTGCACAGATGCAGTGAACGGCTATAC :::::::::::::::::::::::::::::::::	351 GTGCATATG .:::: ATGTAT	3580 AGCCCCTGTGATAATT' .::::::: TACTGCGCTAAT- 1420
Slit 325	Slit 325	Slit 325	Slit 325

Fig. 5M-13

3710 AGTC :.	3780 .rgaa .raa-	3850 GTTC .:.	3920 GAAA
3. 4GA(:::	3. 3AT(3AT(3850 GCGTGTTC :::::: GCAAATAC 1590	35 [GGZ
CAAAG	:: CTTTC	3850 GGCGTGTTC ::::- GCAAATAC 1590	GAJ
37 AAACAAAGAG ::: TTTCTGGGAA	70 3CC2 3CC1	10 3666	10 3AA1 ::::
3700 FATAAZ :: FACTI	3770 ATTGC(:::	3840 ATCGG	3910 CAATCA :::: AAAACA(
3. TTTTA .::: CATTA 1490	::::::::::::::::::::::::::::::::::::::	CTAT	3ACZ .:
GAA	0 CTTCA(:: CAAGA(1540	AAC.	900 3910 GTGGAGACAATCAATGAT :::::::::::::::::::::::::::::::::
3690 3700 37 GTGTGAATTTTATAAACAAAGAG :::::::::::::::-:::-::-:-:-:	3740 3750 3760 3770 378 TTCGGCCTCAGACATAACACTTCAGATTGCCACAGATGA :::.:.:::::::::::::::::::::::::::::::	3810 3820 3830 38 GTGACAAAGACCATATCGCGGTAGAACTCTATC ::::::::::::::::::::::::::::::::::::	3870 3880 3890 3900 3910 3920 CGGCTCTCATCCAGCTTCTGCCATTTACAGTGTGGAGACAATCAAT
TAG.	ATA •••• TTT"	CGGG:	CAG:
GGT	AACA' .:. .GA-T'	Ů . Ů ∪ H	TTACA(.::. GAACT· 1620
3680 AATT	3750 .GACG;	3820 CATA' :: CA	3880 3890 CCAGCTTCTGCCATTTACAG : : : ::: ::: -CTTCTGTTACCTTGAACT- 1610 1620
3 AAA .C	3 CAG :::	3. GACC.: C.	3 TGC::TAC
TGAAZ :: AGAC 1480	0 GGCCT . : ACCTG	AAG : A	CTTCT::::::CTGTT
0 3670 GGGAGAAAGTGTGAAA ::::::::::	3740 TTCGG ::: TTCAC	3810 GTGACAA : . : : : : GAGACTA	3880 CCAGC :::
36 AAAA : : :	37 GTT: ::	38 GTG:	38 TTCC ::
GAGAZ :::: GAAAZ 1470	AAG	AGG	TCA
50 1GGG :: GG	30 16CC	00 TATA :: TA	70 3CTC
3660 ATCAG	3730 TTCAG	3800 TCCTGTAT:::: TCCATTA-	3870 386C
3CTA 	720 CAGATTCCTTCA :::::: CGAATTCCTAC- 1510		4CAC
50 CCTG(::: CCT	720 CAGATTC: :::: CGAATTC:) ATCO) \TGZ \
3650 TGCC	3720 TCAG2 	3790 GGAA	3860 AGCTA' :: TACTA' 600
E I	I CH	4GCC	38 CCAGC: :: CTTAC
3650 3670 3680 3690 3710 3710 AGTGTTTGCCTGGCTATCAGGGAAAAAGTGTGAAAATTGGTTAGTGTGAATTTTATAAACAAAGAGTC ::: :: :: :: :: :: :: :: :: :: :: :: ::	3720 3730 3740 3750 3760 3770 3780 TTATCTTCAGATTCCTTCAGCCTCAGGCTCAGACGACCATACACTTCAGATTGCCACAGATGAA :::::::::::::::::::::::::::::::::	3790 3840 3850 GACAGCGGAATCCTCTGTATAAGGGTGACAAAGACCATATCGCGGTAGAACTCTATCGGGGGCGTGTTC :::::::::::::::::::::::::	3860 GTGCCAGCTATGACA::: AA-CTTACTA
			
slit 325	Slit 325	Slit 325	Slit 325

Fig. 5M-14

 	4060 TGCCAG	4130 CATCCG	4200 CCTGGC
.::::- AGGGAA-	4050 TGTAGGAGGCA	4120 TTCCACGGCTG :: TT	4150 4160 4170 4180 4190 4200 CAGTGAGCTGCAGACTTCCAGAAGGTGCCGATGCAAACAGGCATTTTGCCTGGC ::::::::::::::::::::::::::::
.:::: ATGTC 60	4040 CTCCACTCTA	4110 CGGAACCAGC' : ::: TGCTAGC' 1730	4180 CCGATGCAAA
:: CA 16	4030 .AATTTTGACT .:.::. .GAAGTTGA	4100 CTGGGCAGAA : ::: -TTGACATTT 1720	4170 CCAGAAGGTGC ::: GTG- 1750
 	4020 STCCACTCTG ::::. ACACAA	4090 3GCCAGGCCC	4160 CGCAGGACTT
:.:: TGCTGCTT	4010 GTCAAAGCAC :: GT	4080 GCATCTCTGC :::	4150 ACAGTGAGCTG : ::: TTAGCTT
::::: 325 CTACCGAATGA 1640 16	4000 Slit ATCATCACTAACTI ::::::::::::::::::::::::::::::::::::	4070 Slit GGAAGAGTAACGTG :::::::::::::::::::::::::::::::::::	4140 Slit GAACCTTTACATCAAC ::::::: 325TTTTCATC
	::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	325 CTACCGAATGATGCTGCTTCAATGTCAGGGGAA 1640 4000 4010 4020 4030 4040 4050 4060 Slit ATCATCACTAACTTGTCAAAGCAGTCCACTCTGAATTTTGACTCTCCACTCTATGTAGGAGGCATGCCAG ::::::::::::::::::::::::::::::::::

Fig. 5M-15

4270 TCACCT •	0 4340 CTTGGAAATAA :::::: CAAGGGAAAAT	4410 GCCATGGA :::: ATGTA 1870	4480 CACGGGAAGT :::: CT-AGAAAGT 1910
4260 CAGGCAGGCTTC ::::::	4330 4340 CTTGCCTTGGAAATAA :::::-:	4400 CTTGGAGGGC	60 4470 4480 ATCAAGTGCAAGCACGGAAGT :::::::::::::::::::::::::::::::::
4250 GCCCAGCAGC	4320 ACCAATGACC 	4360 4370 4380 4390 4400 4410 CTGCTTGCCCATCAATGCGTTCTCCTACAGCTGTAAGTGCTTGGAGGGCCATGGA ::::::::::::::::::::::::::::::::::	4430 4440 4450 4460 4470 4480 GAAGAGGATCTGTTTAACCCATGCCAGGCGATCAAGTGCAAGCACGGAAGT : :::::::::::::::::::::::::::::::::::
4240 GCACATGCCA	00 4310 CCTCTGTGACCAACGG : ::::: :: CATCAGAAAACT	4380 TTCTCCTACAG :: :: ::: TTATCAGTCAG 0	4450 TAACCCATGCCA :::: ::: TAACACTTCCC- 90
4230 TGTGCCCATG:	4300 4: GGCCCCTCTGTGA(: ::::: CATCAGAAA)	4370 CATCAATGCGT:	4440 GATCTGTTTA:::
4220 .caagaaggrgrg .:: ::: aaagrrgrr 1780	4290 .GGATGGATGG :: .GG	4360 .ccrgcrrgcc ::: .acagcrr	4430 .TGAAGAGGAG :: TG
4210 4220 4230 4240 4250 4260 4270 TGTGAGCCATGCCACATGCCAGCCCAGCCAGGCAGGCTTCACCT :::::::::::::::::::::::::::::::	4280 4330 4340 GCGAGTGCCAGGAAGGATGGACCCTCTGTGACCAACGGACCAATGACCTTGCCTTGGAAATAA .::::::::::::::::::::::::::::::	4350 Slit ATGCGTACATGGCACO : .: : .: : : : 1325 AGACTTGAATA-CTAO 1830	4420 GGTGTCCTCTGTGAT(. :: ::::: .: ACTG-CCTCAAT-TT(
slit 325	Slit 325	Slit A' : 325 A(1830	Slit 325

Fig. 5M-16

4550	GTGATCG	-TAAACA		4620 4620		V5.T.T.	4690	CCGCTGA	ACTC		4760	AGAAAGT	•••	AAA	
4540	3GGACAGCT	GACTTCA-TAAACA	1940	4610		-6CA-CAGGTC-ATTCTTTTG 1970 1980	4680	STGCTGTGGA	-TGCTTTATAACTC	2000	4750	BACGAGGTTG		TGGACATGATTTAAA	2050
4530	r'GGA'I'ACACG(ATTC		4600		6CA-CAGG 1970	4670	CCCGATTAGAGTGCAGGTGGGTGTGCAGGAGGGCCAGTGCTGTGGACCGCTGA			4740	ATACTCTTTCGAATGCACTGACGGCTCCTCCTTTGTGGACGAGGTTGAGAAAGT	•	 	10
4520	ATGCAGCAG!	1		4590 zadonatran		 	4660	GTGGGTGTG			4730	TGACGGCTCC	•••	TCAGT	2040
4510	CCIACIGIGA	1		4580 Gataagagat		1GAAAA1GAG	4650	GAGTGCAGAG			4720	TCGAATGCAC	•	ATTGTCTATAAGAAACT-	2030
4500	CTGGGGCAGC	GGAGCAG-	1930	4570	•• E		4640	GICCCGAITA			4710	AAATACTCTT	•	ATATTGTCTA	2020
4490 200 kg a a a a a a a a a a a a a a a a a a	SIII GCAGGCIIICAGGICIGGGCAGCCCIACIGIGAAIGCAGCAGIGGAIACACGGGGGGGACAGCIGIGAICG	CCTGGCTT	1920	4560 4570 4580 4590 4600 4600 4600 4600 4600 4610 4620 A620 A620 A620 A620 A620 A620 A620 A		o AAIIGI-ICC 1950	4630	Slit ACAACCAAGAAGGTGT	325 ACATTC	1990	4700	GGAGCAAGCGGCGGAA	•	AACTAA	2010
 	SILT	325) 	32.0 1.0		Slit	325			Slit		325	

Fig. 5M-17

4830	AAGGTTG	•	ATAATTA		4900	AAAATAC	•••	TAA							
4820	ICTTTGGAA	•••	CTTATATAATTA	2070	4890	ATATATTGT	••	ATATGTTTT	7.130						
4810	ACGAGGTGTGTGTCCTAAACACACTCCCGGCAGCTCTGTCTTTGGAAAAGGTTG				4880	ATATTTGAA?		ATTATTAAAP		4950	ATTTG				
4800	ACACTCCCG	••	AAACCTC		4870	ATAGTGGAAA	:	SAGGTTAGC2	0717	4940	TATTATGAGAATAAAGACTTTTTTTTTGCATTTG	••	BCCGC-		
4790	STCCTAAACA	••	AAAC	2060	4860	BATGCTTC		AATTATATG	7777	4930	AAAGACTT	•••	AAGGGCG	2160	
	AGGTGTGTG		!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!			GGACTAATG	•••••••••••••••••••••••••••••••••••••••	AATATAATG 2100	7 100		TATGAGAAI		AAAAAAAAAAAAGGGCG-		
4780	GCTGTACG	••	DID		4850	SACCATGTG	•	TTGGA	7030	4920	ATTTTAT	•	TAAAAAAAA	2150	
4770	Slit GGTGAAGTGCGGCTGT				4840	Slit TATACTTCTTGACCATGTGGGACTAATGAATGCTTCATAGTGGAAATATTTGAAATATATTGTAAAATAC		325 TATACTT-TAGTTGGAAATATAATGAATTATATGAGGTTAGCATTATTAAAATATGTTTTTAA	7080	4910	AGAACAGACTTATTT	••	L	2140	
	Slit		325			Slit		325	7		Slit		325		

				79/109		
11 146	31	51 266	71	91 386	111	131 506
L	C H GC	K AAG	S AGC	N AAT	E GAA	G GGA
	P CCC	K AAG	S TCC	C TGC	S AGC	P CCA
	T ACG	A GCA	E GAG	E GAA	K AAG	SHICH
	P CCG	T ACC	Y TAC	H H H C	Γ	C
	K AAG	D GAC			Q CAG	C TGC
						V GTG
	A GCC					K AAA
	A GCC					CIG
			K AAG			TACA
	PCCG	N AAC	E GAA	L	E GAG	K AAG
	A GCG	T T T	E GAG	9999	$_{ m CTG}$	V GTG
3CC 7	CCC	K AAG	W TGG	E GAG	H CAC	C TGT
ACCC	P CCG	D GAC	A GCT	CIG	E GAG	H H H H H
CGCT/	L	V GTG	T ACG	I ATC	E GAG	W TGG
3CAG(N AAC		Q CAG	E GAG
ומממ		G GGG	GGG	L CIG	A GCG	F TTC
TCT	L CTG	CGG	9 9 0	L CTG	E GAG	$_{ m LTA}$
CTGCC	CTT	C TGC	ტ ტ	R CGC	L CTA	D GAC
30660	P	R CGG	FTTT	I ATT	M ATG	P CCT
GCTC	L	H CAC	N AAC	E GAG	Q CAG	Y TAT
	ユタ	CGC CTG CCG CGG GCC GCG CTG GGG CTC 14 PEANKKPTPC3 G CCG GAG GCC AAG AAG CCG ACG CCC TGC 20	R	R	R L P R R A L G L I	R L P R A A L G L I

Fig. 6A

Fig. 6B

				8	1 /109			
311 1046	331 1106	351 1166	354 1175	1254	1333	1412	1432	
T ACT	V GTG	E GAA		AGT	TLG	AAAA		
N AAT	C TGT	R CGC		CTG	TIG	AAAA		
Y TAC	A GCC	S TCC		TCTC	TTT	AAAA		
ပ္သင္မ	D GAT	CCC		19000	TGCF	CAAZ		
N AAC	E GAA (L CTG		GGAT	CAGC	TAAI		
E N GAA AAC	T ACG	Q CAG		CTGA	TAA	TAGG		
N AAC	E GAA	T ACA		GGCC	וכככו	ATTG		
K AAA	E GAA	P CCG		ATGI	TTGI	GACC		
R AGG	H H T C	S AGC		GAAA	TCAI	AATI		
V GTG	299 8	E GAA		CGTG	ATTC	ATAA		
C TGT	D GAC (G GGA		GTCC	GTTG	TGTA		
T ACC	PCCT	E GAA		GGAT	AACG	TCLI		
	C	T ACA		AGAA	CTCI	CAGI		
E GAA	C V TGT GTG	A GCC		ATTC	TGCI	GATA		
A GCA	C TGT	E GAA		AATT	TGCC	TTTI	7 \	
L CIA	VGTC	A GCT		TTT	AGGC	TAT	AGAC	
S TCA	Y TAC	E GAG		ACCC	GGAG	CTTG	CGCI	
E C S L A E K GAG TGC TCA CTA GCA GAA AAA	S Y V AGC TAC GTC	P A E A E A T CCG GCA GAG GCT GAA GCC ACA	* TAA	GTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGAAAATGTGGCCCCTGAGGATGCCGTCTCCTGCAGT	GACAGCGGCGGGGAGAGGCTGCCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTG	'ICTTAAACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAATTGGACCATTGTAGGTAATCAAAAAAAA	AAAAGGGGGCGGCTAGAC	
E GAG	P G	PCCG	L CTG	35225	AGCG	TAAA	AGGG	
D iAC	P CA	ь СС	D 3AC	GTC	GAC	TCI	AAZ	

Fig. 6C

20 30 40 50 50 ELPPPARVASRKPTMCORCRALVDKFNOGMANTARKNFGGGNTAWEEKSLSKYEF	LLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEEKTLSKYES 20 30 40 50 60 70	\dashv	SDFECNOMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLAC 140 120 130 140	160 170 180 190 200 GDGSRQGDGSCQCHVGYKGPLCIDCMDGYFSLLRNETHSFCTACDESCKTCSGPT	::::::::::::::::::::::::::::::::::::::	230 240 250 260 270 DACVDVDECAAETPPCSNVQYCENVNGSYTCEECDSTCVGCTGKGPANCKECISG	GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISG 230 240 250 260 270	300 310 320 330 340 340 SETKVCKKENENCYNTPGSFVCVCPEGFEE-DRRCLC-TDSRRRSGRGKSHTATL	:. :.: . :::::::::::::::::::::::::::::	
50 GMANTARKNFG	PCHRCRGLVDKFNQGMVDTAKKNFGGGNTAW 0 40 50	120 PNLFEWFCVHTL	::::::::::::::::::::::::::::::::::::::	190 SYFSLLRNETHS	SYFSSLRNETHS 190	260 SYTCEECDSTCV	::::::::::::::::::::::::::::::::::::::	330 FEE-DRRCLC-T	::: . : FEETEDACVPPA 330	
40 ORCRALVDKFNO	HCRGLVDKFNC	110 zawwotlkkeci	.:::::::::::::::::::::::::::::::::::::	180 YKGPLCIDCMDC	YQGPLCTDCMDC 180	250 SNVQYCENVNGS	SAAQFCKNANGS	320 PGSFVCVCPEGI	::::::::::::::::::::::::::::::::::::::	
) ARVASRKPIMC(APEAAKKPTPCI	100 NQLLEQHEEQLI	::::: .::: NQMLEAQEEHLI 100) 170 2GDGSCQCHVG	GDGSCRCHMG 170	240 VDECAAETPPC	VDECAAEPPPC: 240	0 310 CKKENENCYNT	: . ::::::::::::::::::::::::::::::::::	
딛	PLL	80 IMEGLCDSNDFECN	::::::::::::::::::::::::::::::::::::::	CD	•• C)	220 230 XGWTRVEDACVDV	LOE	290 300 ADIDECSLETKVC	:::::: :: ::	
10 C MHLPPAAAVGLE	H MRLPRRAALGLLPLI	70 8 C SEIRLLEIME	H SEIRLLEILEGLCES 80	140 C QGGSQRPCSGNGH	H QGGSQRPCSGNGHCS	210 220 C NKGCVECEVGWTRVE	:.:::::: H NRDCGECEVGWV 220	280 290 C YSKQKGECADIDECS	: :::::::::::::::::::::::::::::::::	C P

Fig. 6E

H EDL

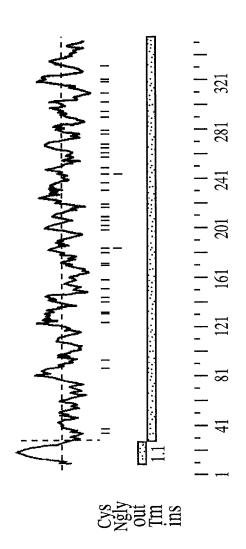


FIG. 6D

10 20 30 40 50 50GCGCTTGCCGGTGGGCGAGGCGAGCT-CCACA :::::::::::::::::::::::::::::::::	60 70 80 90 100 110 C GCAGIT-CIC-TGCCG-GICG-CCCGCGAGIGC-ACCCGCCAIGCACCTGCCGC-CCGCTGCCGCAG : :: :: :: :: :: :: :: :: :: :: :: :: :	120 130 140 150 160 170 180 C TCGGGCTGCTACTGCTGCTGCCGCCTCCCGCGAGCCGACAATGTGCCA :::::::::::::::::::::::::::::::::::	190 200 220 230 240 250 250 240 250 250 240 250 250 240 250 250 240 250 250 250 250 250 250 250 250 250 25
10 20 GTAGCCGGGGGAACGGC-CGGC : .:: .::: ::: ACGCGTCCGCACANGGCCGGCGCGGCTG	70 CTC-TGCCG-GTCG-(::::::::::::::::::::::::::::::::::::	130 140 GCTACTGCTGCTGCCCC :: :::::::: GCCGCTTCTGCTGCTGCTC 50 160	200 210 CGCTGGTGGACAAGTTC. ::::::::::::::::::::::::::::::::::::
CGTAGCCGGG ::: . ::: . H ACGCGTCCGCA	60 C GCAGIT-C : :: : : H GGACCIGGAGC 80	120 C TCGGGCTGC' : :::: :: H TGGGCTCCTGC	190 C GAGGTGCCGGGCGCT ::::::::::::::::::::::::::

Fig. 6F

-1 E)	7h 7h	~ · · · · ·	E. 7)
320 GATT? ::: GATC	390 CTAC :::	460 TGAZ	530 TTG. :: CTG(
3 3GAG 3:::	SCAG SCAC	ACAC	2258 2358 2358
CCTG:::	3GAG(:::: 3GAG(CACA:::	AGAG :::: AGAG
310 : 	380 TGA(::	450 GTA(::.	520 CTC
3 [TCG:::1CG	16CA :::	CTGT	366T
AGA::::	AAC7 GGC-	GTTCT::::	GGTG(::: GGCG(
300 AGTG :::	370 TTGG;	440 4GTG(::::	510 3CAG
270 280 300 300 320 320 320 320 320 320 320 32	330 340 360 360 370 380 390 390 390 390 390 390 390 390 390 360 360 360 360 390 390 360 360 360 390 390 380 380 390 400 400 410	410 420 430 440 450 460 ACTGAAGAAGGAGTGCCCTAACCTATTTGAGTGGTTCTGTGTACACACAC	470 480 490 500 510 520 530 AGCATGCTGTCTTCCAGGCACCTATGGGCCAGACTGTCAGGAATGCCAGGGTGGGT
CGAAL CGAG 320	CAACT	OTATI	0 AGGAA' : : TCGCA' 530
290 GTA(:::	360 'AAC(:: 'AAT(430 'AACC' .:: 'GACT'	500 GTCA
CCAA	ATGC:::	GCCCI ::: ATCCI 450	AGACT :::: CGACT 520
::::::::::::::::::::::::::::::::::::::	TGAAT::::	CGTG	00 3CCA 3CCA 5CC
280 AGTC::	350 ACTT' ::::	420 AGGAG' .::.	490 TGGGC(:::
::: ::: AAG	ACG.	AAGA :::: AAGA(440	CCTA' :::: CCTA' 510
3 3 300	0 AGCAA(::::. AGCAG(370	410 SACTGA .:::	480 .GGCAC :::::
27(GGA(:::	340 GACA ::::	4 ACAG	4 .::: .:::
GCGTG::::::::::::::::::::::::::::::::::	CTGTGT ::::: CTGTGC 360	GCAG::::	CTTC:::TCTC
260 AACACGGC ::::::: AACACGGC	CCT(CT(CT)	400 GGCCTGGTGGCAG ::::::::: GGCCTGGTGGCTG	470 CTGT(::::CTGC'
260 4ACAC ::::	330 GAGGGC ::::: GAGGGG	CCTG 4	ATGC
. : : 666 80	330 340 360 360 370 380 390 390 390 390 330 380 390 390 390 300 300 300 300 300 300 30	400 410 420 430 440 450 460 AGGCCTGGTGGCAGACACTGAAGGAGTGCCCTAACCTATTTGAGTGGTTCTGTGTACACACAC	470 480 500 500 510 520 530 AGCATGCTGTCTTCCAGGCACCTATGGGCCAGGACTGTCAGGGTGGGT
C H	D H	O H	O H

Fig. 6G

A	0 H · · H	0 3.: AA	0 C S C C S C C S C C S C C S C C S C S
600 !AGGA .::.	670 3AGCT:::	740 ::::::	81. 3CTG.
CACG1 ::::: CACA1 620	.:::: .:::: .cccac	GGAG1 :::: CGAG1 760	CCACC :::: CCTCC
590 GTGTC :::::	660 GAGAC ::::: GAGAC	730 ::: :GGGGC	800 GACCC : ::
5 3CAG	6 1.::: 1.4ACG	7 GCTG	8 4GAG :::
CTGC:::	: : : : : : : : : : : : : : : : : : :	.:: .:: .:: .:: .:: .:: .:: .:: .:: .::	. # GGCZ . : : . : GGCC 820
580 GGTC :::: GGTC	650 GCTG :::	720 AACA ::::	790 GTGC :::: GTGC
3ACG :::: 3ACG	U U U	AACC .::: GACC	GAGT:::GAGT
366CG	rrcage::::::rrcage	STCCAL	CGACG
570 3ACAG ::::	640 TACT: ::::	710 CAGG'	780 ATGTT
AGCAG::::	ATGGC : ::: ACGGC 660	ATGC1 .:::	GTGG2 ::::: GTGG2 800
550 560 570 580 600 TGCGACGGAGATGGCAGCACAGGCCGACGGTCCTGCCAGTGTCACGTAGGAT ::::::::::::::::::::::::::::::::	620 630 640 650 660 670 GTATCGACTGCATGGCTACTTCAGCTTGCTGAGGAACGAGACCCACAGCT : ::::::::::::::::::::::::::::::::::	690 720 730 740 TGAGTCCTGCAAGACATGCTCAGGTCCAACCAACAAAGGCTGTGGAGTGCGAA :::::::::::::::::::::::::::::::::	760 770 780 790 800 810 GTGGAGGATGCCTGTGGATGTTGACGAGTGTGCAGCAGCCCCACCCTGCA : :::::::::::::::::::::::::::::::::::
5 AGAT	6 FGCA :::: FGCA	7 3CAA ::::	recc :::
	:::: :::: :GAC!	::: ::: :CCT(166A' ::. 1666 790
550 GCGA :::	620 GTATC : : GCACT	690 GAGT ::::	760 TGG?
CACT:::CACT	TGTG:::TGTG	TGAT::: TGAC TGAC	CGTG
16600 16600 16600	10 GCCGCT ::::: CCCGCT	CCTGT:::::) SACAC : . : 3GTGC 780
540 CGGGAATGGCCA :::::::::: CGGGAATGGCCA 0 570	610 AGGGGC ::::	680 GCACAGCCTGTGA :::::::::: GCACAGCCTGTGA	750 3CTGG :::::
540 560 570 580 600 AGCGGGAATGGCCACTGCCACTGCCACTGCCACTGTCACGTAGGAT ::::::::::::::::::::::::::::::::::::	610 620 630 640 650 660 670 ACAAGGGGCCGCTGTATCGACTGCATGGATGGCTACTTCAGCTTGAGGAACGAGACCCACAGCTT :::::::::::::::::::::::::::::::::::	680 CTGCACAGCCTGTGA ::::::::::: CTGCACAGCCTGTGA 710	750 760 770 780 790 800 810 810 810 810 810 810 810 810 810 810 810 810 810 810 810 820 830 830 810 820 830
C H	C H	O O I	O O K

Fig. 6H

820 830 840 850 860 870 880 GCAATGTACAGTACTGTGAAAATGTCAACGGCTCCTACACATGTGAAGAGTGTGATTCTACCTGTGTGGG ::.::::::::::::::::::::::::::::	890 910 920 930 940 950 CTGCACAGGAAAAGGAGAGTGTATCTCTGGCTACAGCAAGCA	960 970 1020 GCAGATATAGATGCTCATTAGAAACAAAGGTGTGTAAGAAGGAAAATGAGAACTGCTACAATACTC ::::::::::::::::::::::::::::	1030 1040 1050 1060 1070 1080 1090 CAGGGAGCTTTGTCTGCGTGTGTCCGGAAGGTTTCGAGGAAGACAGAC
C GCAAT :::: H GCGCT 840	C CTGCA ::::: H CTGCA 910	C GCAGA ::::: H GCAGA 980	C CAGGG ::::: H CAGGG

Fig. 61

rig. of

79	158	16 220	36	56 340	76	96 460	116 520	136 580
BCTG	CCCT	Q CAG	R CGC	CCT	R CGG	V GTG	S TCG	GGC
rgca(CAG(A GCC (H H H H	I ATC	P CCG	G GGA	A GCG	Y TAT
:AGC:	ACCC	L CTG (A GCT	T ACC	S TCT	R CGG	P CCA	I ATC
FTCT(YCCC7	V GTC	CGC	L	G GGC	A GCG	Y TAC	G GGT
GCAC	ZBDBX	L CTG (D GAC	A GCC	L CIG	V GTG	A GCG	S TCA
CGCC	TGCC	A GCC (EGAG	0 0	V GTG	L CIG	PCCT	D GAC
TCIC	GCAG	A GCA G	S TCA	ე ლე	A GCT	V GTG	L CIG	N AAC
GCAG	CTTC	L CIG	S AGC	CIC	R	EGAG	A GCA	P CCC
TCGC	CAAZ	L CTG (D GAC	V GTG	CGC	A GCA	V GTG	CGC
ACGC	GCGA	P CCC C	GGA	GGC	S AGC	E GAG	R CGC	L CTG
CCTC	AGGAG	L CTG (E GAA	Q CAG	P	R CGG	H H H C	E GAG
CTCI	;cee <i>t</i>	F TTC (L	L CTG	P CCG	g GGC	R CGG	S AGC
CAGC	יבככנ	L CTG 1	V GTT	P CCA	P CCA	R CGG	Y TAC	L CTG
39000	GAGZ	Q CAG (D GAT	A GCG	R CGG	S	A GCC	A GCG
TGC	GGAC	A GCC (A GCA	D GAC	L CIG	L CIG	E GAG	L CTG
GTC	ACC	M ATG (L TTA	g GGC	Y TAC	H H H C	N AAC	S TCC
GICC	GTGC		A GCT	A GCG	H CAC	T ACT	V GTG	V GTC
ACGC	BAGCC	TGC	A GCA	I ATC	V GTC	M	K AAG	D GAC
ST C GACCCAC G C G C C C C G C C C C C C C	ZAGGACTGAGCCGTGCACCCGGAGGAGCCCCCGGAGGAGGCGACAAACTTCGCAGTGCCGCGACCCAACCCAGCCCT	SGGTAGCCTGCAGC	PCCT	R CGC	H CAC	K AAG	V GTC	T ACC
TCC	AGC	3661	A	V STG	ပ္ပင္သ	V STC	G R	CH C

Fig. 7A

				90	/109		
156 640	176	196 760	216 820	236	256 940	276 1000	296 1060
G GGG	Q CAG	Y TAC	CCC	N AAC	N AAT	Y TAC	GGT
K	A	A	Y	R	L	A	D
AAA	GCC	GCC	TAT	CGG	CTA	GCG	GAT
V		A	R	V	D	R	W
GTC	GGG	GCC	AGG	GTC	GAC	CGG	TGG
K	SHU	Y	V		E	A	A
AAG		TAT	GTG	GGG	GAA	GCA	GCC
V GTC	표 표 표	CIC	T ACC	CCC	A GCT	E GAA	A GCA
E	S	Q	Q	F	Y	E	Y
GAG	HCC	CAG	CAG	TTC	TAT	GAG	TAT
V GTG	T T C	E GAG	D GAT	G GGC	C TGT	Γ	$_{ m CTG}$
A	A	P	S	D	YTAC	T	Q
GCT	GCT	CCG	TCG	GAT		ACA	CAA
D	Y	T	L	M	V	L	g
GAC	TAT	ACC	CTG	ATG	GTG		gga
S	R	A	W	D	D	K	T
AGC	CGC	GCC	TGG	GAC	GAT	AAG	ACG
S	A	I	9	G	Y	E	T
AGC	GCC	ATC	99C	GGA	TAT	GAG	ACC
D GAC	STCT	H CAC	A GCT	Y TAC	CIC	P CCA	A GCC
D	ဗဗ	A	D	C	D	P	I
GAT		GCC	GAT	TGT	GAC	CCT	ATT
I	E	G	C	A	D	D	E
ATC	GAG	GGA	TGT	GCC	GAT	GAC	GAG
9 9 0 0	R CGA	I ATT	Q CAA	E GAG	PCCG	G GGT	A GCA
H	Y	R	E	R	D	L	G
CAC	TAC	CGC	GAG	CGA	GAC	CTG	GGT
Q CAG	CIC	A GCC	Y TAT	PCCA	V GTG	F TTC	R CGG
V GTC	다 다 다 다	C TGT	g GGC	TACC	V GTG	LCTG	E GAG
E	V	A		Q	GGT	E	Q
GAG	GTC	GCC	GGG	CAG		GAA	CAG
C TGT	V GTC	E GAG	CIT	I ATC	Y TAT	GGA	C TGC

Fig. 7B

396 1360 416 1420 316 336 1180 376 1300 456 1540 356 1240 436 V GTC CCC S TCG GGA A GCC GGT T ACA E I ATC F D GAC D GAT E GAA GGA E GAA E GAA CCC S TCT Q CAG GGA F TTT EGAG CHC R CGA Y TAC FTC D GAC E GAA L TTG FTTC A GCC PCCT GGC GGC E GAG C TGC L L CTA A GCA LCIC P CCA YTAC K AAG VGTG TACT N AAC Q CAG M ATG LCIC K AAG I ATC TACG GGT S AGT V GTC S TCC L CTG N AAC R AGG 9 99 9 A GCC PCCC E GAA V GTC E GAA D GAT E GAG I ATC E GAG GGT GGT F TTC P CCA PCCT L CIG E GAA A GCT CGC N AAC S TCC A GCC PCCT E GAG S TCA L CTA Y TAC L S AGC S TCC TACC W TGG H CAC E GAG I ATC F TTC G GGC A GCC A GCA 9 9 9 9 . G G G K AAG E GAG A GCC P CCA G GGG T ACA T ACG N AAT GGT VGTG GGG D GAC P CCA PCCT S AGC P CCC E GAA PCCC I ATC T ACA R CGT $^{\rm C}_{
m TGT}$ F PCCG C TGC GGC GGC A GCC V GTC S P CCA H CAC Q CAG GGC E GAA TACT V GTA I ATC S TCT M ATG T ACT D GAC S AGC S TCC PCCT A GCT S AGT L CTG S TCC PCCC Q CAG Q CAG E GAG E GAG S AGC N AAC A GCC G GGA Q CAA GGC T ACA L CTA T ACA

Fig. 7C

Fig. 7D

						/109			
636 2080	656 2140	672 2188	2267	2346	2425	2504	2583	2662	2730
A GCC	A GCC		9991	GAC	CCI	225:	GAG	GGA	
D S A GAC AGC GCC	T ACT		CTAI	CACI	CAGG	rgrgı	CCAG	SCCTI	
D GAC	S TCA		CTAC	Saag	ATCCI	GCC1	3GAG1	ACAAG	7.)
TACT	999		SACCI	SAGCO	BAGCZ	CATCO	TCCC	SAAAZ)5));
V Q A Q P V L P T GTG CAG GCC CAG CCA GTG CTG CCC ACT	P A S G N S A Q G S T CCC GCA TCA GGT AAT TCT GCC CAA GGC TCA ACT	* TGA	racco	ATCC	CACAC	CTTC	ZAACC	SATGO	36060
L CIG	A GCC	P L Q L W V T * CCC CTG CAG CTC TGG GTC ACC TGA	CICL	rgr <i>g</i> z	3000	ACTC	CCT	STTTC	AAAGO
V GTG	S TCT	V GTC	CATTC	ACCCI	3CCA(CACTA	rcaco	SACTO	AAAA
P CCA	N AAT	M TGG	CTT	CTTT	CTC	TTC	CTTC	rttr(AAAA!
Q CAG	GGT	CIC	rttG(3CGT(CACA	CTAT	STCC	[ATT]	AAAA!
A GCC	S TCA	Q CAG	TCCI	CTCC	GCT	GGCC	3GGA(SAAGI	AAAA
Q CAG	A GCA	L CTG	CCT	AGCTO	CTGT	GCT	SCCTO	CTGT	AAAA!
V GTG	PCCC	CCC	ACTCI	rctc2	CACC	rcago	GAAC	ACTTO	AAAA.
S TCA	VGTC	F TTC	CCAAA	GGTA	CCTO	SCCTI	rcago	AACTA	ACCA!
T ACC	V GTG	F	ZATCO	rgrg	regec	rgcad	SATCI	AAGC?	rgta <i>i</i>
G GGG	A GCC	L	CATO	ACCTI	CATI	CTATI	rATTC	CTTZ	CTT
A GCA	V GTG	CIC	CCAC	ATCCA	CTG	rcaco	CICCI	AGAGO	AACCO
PCCA	G GGA	L CTA	rtaa(3GAT	CTTC	CTCAI	TGC	CAC	\TTA
R T A P A G T S AGA ACT GCC CCA GCA GGG ACC TCA	S R G G V A V AGC CGA GGT GGA GTG GCC GTG	L S I L L L F F CTC TCT ATC CTA CTC CTT TTC TTC	CCTGTAGTCCTTTAACCCACCATCATCCCAAACTCTCTGTCCTTTGCCTTCATTCTTTACCCACCTCTACCTATGGG	ICTCCAATCTCGGATATCCACCTTGTGGGTATCTCAGCTCTCCGCGTCTTTACCCTGTGATCCCAGCCCCGCCACTGAC	CATCTGTGACCCTTCCCTGCCATTGGGCCCTTCCACCTGTGGCTCACATCTCGCCAGCCCCACAGAGCATCCTCAGGCCT	CTCCAAGGGTCCTCATCACCTATTGCAGCCTTCAGGGCTCGGCCTATTTTCCACTACTCCCTTCATCGGCCTGTGTGCC	STCCCCTTTAGCTGCCTCCTATTGATCTCAGGGAAGCCTGGGAGTCCCTTCTCACCCCTCAACCTCGGGAGTCCAGGAG	AACCCGTACCCCCACAGAGCCTTAAGCAACTACTTCTGTGAAGTATTTTTTGACTGTTTCATGGAAAAAAAGCCTTGGA	aataaatctctattaaaccgctttgtaaccaaaaaaaaaa
T ACT	R CGA	S TCT	TAG	CAA	TGTC	ZAAGO	CCT	CGTZ	1AAT
R AGA	S AGC	CHC	CCTC	rcro	CATC	CICC	3TC(AACC	AAT?

Fig. 71

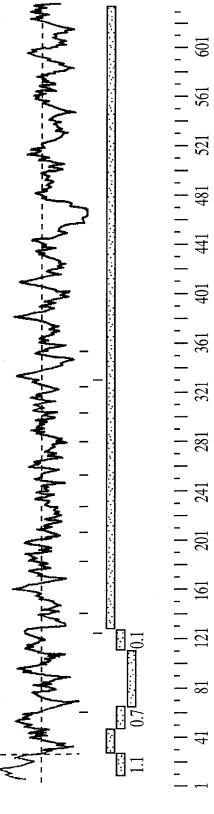


FIG. 7F

Negys In The Negys In The Negys

O 4.	d'. O	00.00	0 Q · W	0 % %	0 4 4
71 SRR	:::: SRRA 70	140 CEVQ ::::	210 VLSD :SS	280 CQER :::: CQER 220	350 RFNV :::: RFNV 290
PPP	· · 선 · · 선	IYR(::: IYR(OAG	AAYC	35 KHSRFN :::::: KHSRFN 290
YLR	::: YLR	DSG .:: DSG	じ り 日	EEA] ::: EEA]	FPNI :::
60 HVH!	09 :::	130 RPN:::	200 GGY	270 KLTL :::: KLTL 210	340 PNQTG: ::::: PNQTG] 280
IPC	·· DA	135. 13 13	AYL	, ・・・ ・・・ ・ ・ ・ ・ ・ ・ ・ ・ ・ ・	 FPN
SALT	::::	SLAI :::: SLAI)LYA	.:: .::	
50 VLG(.:: VLG(50	120 TDVS:::	190 200 210 IATPEQLYAAYLGGYEQCDAGWLSD :SS	260 ELFI :::: ELFI 00	330 PGVKT ::::: PGVKT
ĽQĞ	::: I.QG	ASL	HIA.	LNGE LNGE	SLPC SLPC
DAP	::: DAP	AYP AYP	IGA	AED AED	
40 XIAG	::: XIAG 40	110 :::: :VALP	180 QEACARIGAH 	250 VYCY VYCY 90	320 VTPSQRCGGGLPGVKTL ::::::::::::::::::::::::::::::::::::
FRVE	FRVF	AFRA SFRV	1 10EP	2 'YDV' 'YDV' 19	32 IVTPS ::::: IVTPS 260
DRA.	::: DRAI	EAYI ::: EAYI	FSG7	PDDI ::::	3 Y P J
20 30 40 50 50 70 QAPAALADVLEGDSSEDRAFRVRIAGDAPLQGVLGGALTIPCHVHYLRPPPSRRA	::: SSE 30	90 100 100 140 REAEVLVARGVRVKVNEAYRFRVALPAYPASLTDVSLALSELRPNDSGIYRCEVQ ::::::::::::::::::::::::::::::::::::	170 YAFS	230 240 250 260 270 280 GDMDGFPGVRNYGVVDPDDLYDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQER ::::::::::::::::::::::::::::::::::::	300 340 350 350 330 340 350 350 340 350 350 340 350 350 340 350 350 340 350 350 340 350 350 340 350 350 350 350 350 350 350 350 350 35
EGD	:: EGD	1 3VRV ::: 3VRV	1 ARY	24 .NYGV :::: .NYGV 180	31 LADG:::: LADG 250
ADVI	::::	/ARG ::::	(王GS)	GVR :::	PGW:::
20 AALA	::: AAL/ 20	90 EVL\ :::: EVL\ 90	160 VFLYF 	230 MDGFE ::::: MDGFE	300 LDHCS ::::: LDHCS
QAP	OAP.	REAL ::: REAL	1 GVV]	23 GDMD :::: GDMD	30 3GLD:::36CLD:240
VLA	::: 'VLA	.::: .::: .SRG	KVK	ACY ::: ACY	AWD(::: AWD(
LO JAAI	AAI.	30 ITFI ITFI	00 1VEV 1.: 1VE-	0 PRE PRE	0 LYA ::: LYA
LPLI		SVKW SVKW SVKW	15 35 DP 35 DP 15	22 2101 2101 160	29 11.60 11.60 230
OLF	:: G	6.5. FP		VRYI :::	E T P I
		•		Q	
332	B F F	332 BEF	332 BEF	332 BEF	332 BEF
10 332 MAQLFLPLLAALVLA	::::::::::::::::::::::::::::::::::::::	80 332 VLGSPRVKWTFLSRG ::::::::::::::::::::::::::::::::::::	15 32 HGIDDSSDA :::::::: EF HGIDDSSDA 15	2 QTVRYPI : :::: F QRYPI	290 332 GAEIATTGQLYAAWDO ::::::::::::::::::::::::::::::::::::

Fig. 7G

	YSIPIMEDGGGG 350	480 ::::::::::::::::::::::::::::::::::::	550 LPTPRERNLASPSPSTL:::::::::::::::::::::::::::::::::	580 590 600 610 620 SGVPRGESEETGSSEGAPSLLPATRAPEGTRELEAPSEDNSGRTAPAGTSVQAQP :::::: SGVPRGGARGARTQ-	
370 380 390 400 410 ASNPASNPASDGLEAIVTVTETLEELQLPQEATESESRGAIYSIPIMEDGGGGS	EATESESRGA 340	440 450 460 470 480 ETQSMVPPTGFSEEEGKALEEEEKYEDEEEKEEEEEEVEDEALWAWPSELS:::::::::::::::::::::::::::::::::::	540 PRVHGPPTET ::::::::: PRVHGPPTET 480	610 EGTRELEAPSEDNS ::: -GAR	
390 TETLEELQ	 TETLEELQ 330	460 EEEEKYED: :::::::::::::::::::::::::::::::::::	DGE DGE	600 SLLPATRAP	60 670 ILLLFFPLQLWVT :.: FAL
380 SDGLEAIVTV		450 SFSEEEGKALE ::::::::::::::::::::::::::::::::::::	520 RAVLQPGASPLP ::::::::::: RAVLQPGASPLP 460	590 TIGSSEGAPS	660 STALSILLLE
	 PTQPPTQL- 310	440 EFETQSMVPPTC :::::::::::::::::::::::::::::::::::	510 SLSQAPA ::::::: SLSQAPA 450		650 /VPASGNSAQGSTALS
360 YCFRDSAQP-SAIPE		420 430 332 TPEDPAEAPRTLLEF :::::::::::::::::::::::::::::::::::	0 GPEASLPTEPAAQEK :::::::::: GPEASLPTEPAAQEE 0	560 332 VEAREVGEATGGPEL ::::::::::::::::::::::::::::::::::::	0 VLPTDSASRGGVAVV
332 YCF	BEF YCE	420 332 TPE ::: BEF TPE 360	490 332 GPE ::: BEF GPE 430	560 332 VEA ::: BEF VEA 500	630 332 VLE BEF

Fig. 7H

PPRSRRA :: ::: PPPSRRA	SVYRCEVQ .::::: SIYRCEVQ 140	DAGWLSD::::::::::::::::::::::::::::::::::::	0 EEARDYCLER ::::::::::::::::::::::::::::::::::::	KQNRFNV :::: KHSRFNV 350
60 AIPCHVHHLF .:::::::: TIPCHVHYLF 60	130 LSELRPNDSG :::::::: LSELRPNDSG	200 AAYLGGYEQC :::::::: AAYLGGYEQC 200	270 PPSKLTWEE? :: :: ::: PPEKLTLEE? 270	340 LFPNQTGFPS :::::::: LFPNQTGFPN
50 QLRGVLGGAL .:.::::: PLQGVLGGAL 50	120 PASLTDVSLV :::::::: PASLTDVSLA 120	180 190 200 GAQEACARIGARIATPEQLYAAYLGGYEQCDAGWLSD::::::::::::::::::::::::::::::::::::	260 DLNGELFLGA :::::::: DLNGELFLGD 260	330 GGLPGVKTLF :::::::: GGLPGVKTLF 330
30 40 50 60 DSSEDRAFRVRI-GAAQLRGVLGGALAIPCHVHHLRPPR ::::::::::::::::::::::::::::::::::	110 YRFRVALPAY :::::::: YRFRVALPAY 110	180 GAQEACARIG :::::::: GAQEACARIG 180	250 DLYDVYCYAE :::::::: DLYDVYCYAE 250	320 PIITPSQRCG ::::::::: PIVTPSQRCG 320
DLKE : VLEG	90 100 110 120 130 REVEVLVARGLRVKVNEAYRFRVALPAYPASLTDVSLVLSELRPNDSGVYRCEVQ ::.::::::::::::::::::::::::::::::::::	160 170 180 190 200 GGVVFLYREGSARYAFSFAGAQEACARIGARIATPEQLYAAYLGGYEQCDAGWLSD ::::::::::::::::::::::::::::::::::::	230 240 250 260 270 GDMDGYPGVRNYGVVGPDDLYDVYCYAEDLNGELFLGAPPSKLTWEEARDYCLER ::::::::::::::::::::::::::::::::::::	300 340 GGLDRCSPGWLADGSVRYPIITPSQRCGGGLPGVKTLFLFPNQTGFPSKQNRFNV ::::::::::::::::::::::::::::::::::::
10 M MIPLLLSLLAALVLT : .:.:::::: H MAQLFLPLLAALVLA 10	70 80 M APGFPRVKWTFLSGD .::::::::	140 150 M HGIDDSSDAVEVKVK :::::::::::::::::::::::::::::::::	210 220 M QTVRYPIQNPREACS ::::::::::: H QTVRYPIQTPREACY 220	280 290 M GAQIASTGQLYAAWN :::::::::::::: H GAEIATTGQLYAAWD 290
M H	N H	H Z H	NZ H	7 A H

Fig. 71

0 360 400 410 YCFRDSAHPSASSEASSPASDGLEAIVTVTEKLEELQLPQEAMESESRGAIYSIPISEDGGGGSST ::::::::::::::::::::::::::::::::	420 430 440 450 460 470 EDPAEAPRTPLESETQSIAPPTESSEEEGVALEEEERFKDLEALEEEKEQEDLWVWPRELSSP- :::::::::::::::::::::::::::::::::::	480	610 620 630 640 650 660 670 AQPVLPTDSASHGGVAVAPSSGDCIPSPCHNGGTCLEEKEGFRCLCLPGYGGDLCDVGLHFCSPGWEAFQ :::::::::::::::::::::::::::::::::::
350 36 M YCFRDSAHPS; ::::::: H YCFRDSAQPS; 360	420 M PEDPAEAPR ::::::: H PEDPAEAPR	480 MLPTGS ::: H PEASLPTEP 50 MAREVGG :::: H LVEAREVGE 560	610 M AQPVLPTDS :::::::: H AQPVLPTDS 630

Fig. 7J

740	SDGAPLLY	•	 	810 RPRLRYAV	 	880	APLTPPSS	 	
730	DRTIEGDFLW			800 PQLPLAQIFG	PLQ	870	PKGQLSKHKK		
720	KYREYQWIGLN	••	 660	790 KMGLVSCGPP	 	860	KALKSMDAPEG		
710	LPEEQDFVNDF			780 VPCNYHLSYTC	 	850	ZISCVPRRPGF		
700	ALGAHLTSIC	::	 - - - - - - -	770 VWHDQGQWSDV	; 	840	CQENGLWEAP(:: .	LWVT 670	
069	SWEEAESOCR			760 FLSGENCVVM	[±4	830	LAQKNLPLLK		
089	M GACYKHFSTRRSWEEAESQCRALGAHLTSICTPEEQDFVNDRYREYQWIGLNDRTIEGDFLWSDGAPLLY			750 760 770 780 790 800 810 M ENWNPGQPDSYFLSGENCVVMVWHDQGQWSDVPCNYHLSYTCKMGLVSCGPPPQLPLAQIFGRPRLRYAV		820	M DTVLRYRCRDGLAQRNLFLIRCQENGLWEAPQISCVPRRPGRALRSMDAPEGPRGQLSRHRRAPLTPPSS		
	-		二	4	耳	•	<u></u> 1	出	

Fig. 7K

∵ ∵ ∪ H :• H	0 GCGA :::: GCAA	υ υ ο	A 0	A : D
50 :::	120 3AGGCGA :::: GCAA	190 CTGCC ::::: CTGTC	260 AGCTCA(::::.	330 ;ccrc :::
CTCGC::::	3GAGC	rgirc :::: rgcii	AGACA ::::: AGACA	66666 :: :: 66766
20 30 40 50 CGTCCGTCCTGCGGCCCCCAGCCTCTCCTCACGCTCGCGCAGTC :: :: :: :: :: :: :: :: :: :: :: :: ::	60 70 80 90 110 120 TCCGCCGCCGCAGGAGCCCCCGGAGGAGCCCCCCGGAGGAG	130 140 150 160 170 180 190 CAAACTTCGCAGTGCCGACCCAACCCCAGCCTGGGTAGCCTGCAGCATGGCCCAGCTGTTCCTGCCC ::: ::: ::: ::: ::: ::: ::: ::: :::	200 210 260 260 260 240 250 260 260 CTGCTGCCAGCTCTTAGCAGATGTTCTGGAAGGAGACAGCTCAG ::::::::::::::::::::::::::::::::::::	80 320 330 GCGTGCGCATCGCGGGCGACGCGCCACTGCAGGGCGTGCTCGGCGGCGCCCTCAC :::::::::::::::::::::::::::::::::::
4 CTCCT : ::	1 GAGAC :::: GGGAC 120	1 GGCC :.	2 :CTGG ::::	3 37GCT 31GCT 31GCT
3CCTC :::3 5CC-C) 3GAGG 3GAGG	0 AGCAI :: :: AGAAI 150	0 ATGTT::::ATGAC) 5GGCGT(:::::: 5GGCGT(290
30 cccAGccT ::::::	100 ACCCG :::: GCGCG	170 CTGCA :::: -TGCA	240 GCAGA ::::: GCTGA	310 TGCAG
.: :: ::6cG	GTGCA(:::.	O GGTAGC .::. AGTG	TTTA: : CCTC	CCAC
20 GTCCTGCGGC ::::: GTCCCGCGCG	0 80 110 G-CTGCAGCTGCAGCCGTGCACCCGGAGGAGCCCCC : :::::::::::::::::::::::::::::::	160 CCCTGGGTAG .::. AGTG-	230 SCAGCT	300 1::: 1:::
G1 :: TGGG1	SACTC ::: SACG1 100	4GCCC	CCCTC	36CG/ :: TGC
TGTCT	80 GCAG(:::	150 ACCCC :: TC	220 ::::: :caagco	80 290 GCGTGCGCATCGCGGGC :::::::::::::::::::::::::::::::
cgrcc- :: :: gececcc	AGCT::GGCT	150 :::: CATC	2 	2 GCAT ::::
c .: 	.::: ::::	CGAC	CCTG	0 CGTGC ::::: CGTGC
ı Ü	70 ICAG- :::: ICGGJ	140 IGCCG	210 CTGGT ::::: CTGGT	280 TTCGC: TCCGC
10 :: ::::::::::::::::::::::::::::::::::	AGTC:	GCAG'	200 2 CTGCTGGCAGCCCTG :::::::::::::::::::::::::::::::::	270 AGGACCGCGCTTTTC ::::::::: AGGATCGAGCCTTCC 250
ACCCA .:::.; crcccG	35325 :::: ::::	130 CAAACTTC ::: -GTTCTTC 30	200 CTGCTGGCAGCC ::::::::::::::::::::::::::::::::	270 ACCGCGATCGAGATCGAG
GTCG ::: GAGG	60 70 TCGCCGCAGTCTCAG :::::::::::::::::::::::::::::::::::	. CAAA I -GTI 130	CTGC	AGGA :::: AGGA
H Z	Η Σ	H Z	H Z	Η Σ

Fig. 7L

		•	
400 ccccccccrc :::::: ccccccccrc	470 TCAAGGTGA ::::::: TCAAGGTAA 0	540 :::::::: TCTAGTATT 0 610 GACAGCAGC :::::::	680 ATGCTTTCT ::::::: ATGCTTTCT 0
340 350 360 400 CATCCCTTGCCACGTCCACTGCGGGCCACCGCGGCCTGTGCTGGGCTCTCCGCGGGTC ::::::::::	410 420 430 440 450 460 470 AAGTGGACTTTCCTGTCCCGGGGCCGGGAGGCAGAGGTGCTGGTGCGCGGGGAGTGCGCGCGTCAAGGTGA ::::::::::::::::::::::::::::::::	480 490 500 510 520 530 540 ACGAGGCCTACCGGTGCCTGCCTGCCTCCCCGCTCCCCGACGTCTCCCTGGCGCT :::::::::::::::::::::::	30 640 680 AAGGTCAAAGGGGTCGTCTTTCTCTACCGAGAGGGCTCTGCCCGCTATGCTTTCT :::::::::::::::::::::::::::::::
380 cceeecrere ::::::: cceeecceee	450 GTGGCGCGGG ::::::: GTGGCTCGCG	520 CGTCGCTCAC : : : : : : : : : : : : : : : : : : :	660 CGAGAGGGCT(:::::::: AGAGAGGGCT(640
370 GCCGAGCCG ::::: GCGCAGCCG	440 GAGGTGCTG :::::: GAGGTTCTG	510 CGTACCCAG(:::::: 490 580 TCGCTGTGA(:::::::	650 TTTCTCTAC(:: :::: TTCCTCTACA
360 GCGGCCACC :::::::::::::::::::::::::::::	430 CCGGGAGGCA ::::::::::::::::::::::::::::	500 :cacrdccrd :cacrdccrd 480 570 AGGTATCTA :cgGGGTCTA	640 .GGGGTCGTC :::::::::: .GGGGTCGTC
350 rccactacci :::::::::::::::::::::::::::::::::::	120 STCCCGGGGC ::::::::::::::::::::::::::::::	490 GTTCCGCGTGG :::::::::::::::::::::::::::	330 :aaggtcaap :::::::::::::::::::::::::::::::::::
10 CTTGCCACGI :.:::::::	-0 	480 ACGAGGCCTACCGGT ::::::::::::::::::::::::::::::::::	620 GACGCTGTGGAGGTC :::::::::::: GATGCTGTGGAGGTC 90
340 H CATCCCT :::::: M CATCCCA 310	410 H AAGTGGA :::::: M AAGTGGA 380	480 H ACGAGGCCTAC ::::::::: M ACGAAGCCTAC 450	620 H GACGCTG ::::: M GATGCTG

Fig. 7M

U ·· U U ·· U U ·· U	(¹) • ✍¹
750 CTCTATG CTCTATG 820 ATCCCAT 	970 980 1000 1010 1020 1030 TCCAGAGAAGCTGACATTGGAGGAAGCACGGGCGTGCAGAGATTGCCACCACG ::::::::::::::::::::::::::::::
740 CGGAGCAG CGGAGCAG 720 810 CGTGAGGT 790 R80 AACTATGG ::::::: AACTATGG AACTATGG 860 950 1GTTCCTG 1GTTCCTG	1020 CAGAGATTG : ::: : CACAGATCG
GCCACCCC 3	1(GGGGTGCZ ::::: GTGGTGCZ 990
730 CCCACATC CCCGAATC 700 GCTGTCGG :::::::: 770 TTCCCGG 770 TATCCTGG 840 840 840 ACCTAAATC 840 ACCTAAATC 940 ACCTAAATC	1010 CCAGGAGCC :::::: TCTGGAACC
720 ATTGGAGC ATAGGAGC 790 TGGCTGG :::: 860 SGATGGCT 3GATGGT 3GATGGT 3GATGGT 3GATGGT 3GATGGT 3GATGGT 3GATGGT 3GATGGT 3GATGGT 3GATGGT 3GATGT 3	1000 CGTACTGC :::: ACTACTGT
GCCCGCZ GCCCGCZ GCCCCCZ 690 GTGATGC :::::: GTGATGC 760 AGACATC :::::: AGACATC 161TATC 161TATC 161TATC	0 CACGGGG ::::: CTCGGG7
710 GGCCTGTG 680 780 GAGCAATG 1850 750 GTTACGGA 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	990 GAGGAAGC ::::::: GAGGAGGC 960
700 CCCAGGA CCCCAGGA 770 GGGCTAT ::::: CGGCTAT GAGGCCT CTATGA TCTATGA TCTATGA	980 GACATTG :::::: GACATGG
690 TTCTGGGGG :::::: CGCTGGAGG 760 TACCTTGG 130 830 CCCCACGAG 131 810 810 810 810 810 810 810 810 810 81	970 GAGAAGCT(. ::::: AGCAAGCT
H CCTTT 660 7 H CGCCT 730 730 R CAGAC :::: M CAGAA 800 H ACCCG 81:: M CAGAA 800 800 1::: M CAGAA 800	9 H TCCAG ::: • M TCCCA

Fig. 7N

040 1050 1060 1070 1080 1090 AACTGTATGCAGCCTGGATGGTGGCTGGACCAGGCCCAGGGTGGCTAGCTGAT ::::::::::::::::::::::::::::::::::::	1260 1270 1280 TGCCATCCCTGAGGCCTCCAACCCAGCCTCCAACC :::::::::::::::::::::::::::::	AATCCC::::
---	--	------------

Fig. 70

1390 1400 1410 1420 1430 1440 1450 CATCTACTCCCATCATGGAGGAGGAGGAGGTGGAAGCTCCAGCAGAGCCCAGCAGGGGCC :::::::::::::::::	1460 1470 1480 1490 1500 1510 1520 CCTAGGACGCTCCTAGAATTTGAAACCAATCCATGGTACCGCCCACGGGGTTCTCAGAAGAGGAAGGTA	1530 1540 1550 1560 1570 1580 1590 AGGCATTGGAGGAAGAAGAAGAGAAGAAGAAGAAGAAGAAGAAG	1600 1610 1620 1660 GGAGGATGAGCCCCAGCGAGCTCAGCAGCCCGGGCCCTGAGGCCTCTCTCCCCCACT ::::::::::::::::::::::::::::::::::::	1670 1680 1690 1710 1720 GAGCCAGCCAGCCAGGAGGCCAGCCTGCTGCTGCTGCTGCTGTG : : : : : : : : : : : : : : : : : : :
1390 1400 H CATCTACTCCATCATC :::::::::::::::::::::::	1460 1470 H CCTAGGACGCTCCTAGAATTTC :::::::::::::::::::::::::::::::::	1530 1540 H AGGCATTGGAGGAAGAGAGAA: :::::::::::::::::::::::::::::::::	1600 1610 H GGAGGATGAGGCTCTGTGGGCZ ::::: M GGAGGAC-CTGTGGGTC	1670 1680 H GAGCCAGCAGCAGAAGT : :: :: :: :: : : : : : : : : : : : :

Fig. 7P

1750 1760 1770 1780 1790 ATGGAGAGTCAGACCTTCCAGGCCTCCAAGGGTCCATGGACCTACTGAGAC ::::::::::::::::::::::::::::::::::	800 1810 1820 1830 1840 1850 1860 TCTGCCCACTCCCAGGGAGCAACCTAGCATCCCCATCCACTTCCACTTGAGGCAAGAGGTG :::::::::::::::::::::::::::::::	870 1880 1890 1900 1910 1920 1930 GGGGAGGCAACTGGTCCTGAGGTCCCTCGAGGAGAGGAG	1940 1950 1960 1970 1980 1990 2000 HGAGGGTGCCCCTTCCCTGCTTCCAGCCCCACGGGCCCCCTGAGGGTACCAGGGAGCTGGAGGCCCC ::::::::::::::::::::::::::::::	2010 2020 2030 2040 2050 2060 2070 CTCTGAAGATAATTCTGGAAGAACTGCCCAGCCCAGCCC
1750 ATGGAGAGTCAG	1820 GGGAGAGGAACCT:::::::::::::::::::::::::::	1890 GGTCTGAGCTA' : :::::: NGCCCTGAGCTC' 1790	1950 1960 CTTCCCTGCTTCCA(:::::::::::::::::::::::::::::::::	2020 2030 TGGAAGAACTGCCC :::::::::::::::::::::::::::::::::
1730 1740 H CATCACCACTTCCTGA :::::: M CGTCACCTTCTCCTG 1670	800 1810 1820 TCTGCCCACTCCCAGGGAGGAACC : :::::::::::::::::::::::::::::::::	1870 1880 GGGGAGGCAACTGGTG :::::::::::::::::::::::::::::::::	1940 GAGGGTGCCCC:::::::::::::::::::::::::::::	2010 :AAGATAATTCT :::::::::::::::::::::::::::::::
1730 H CATCA ::::: M CGTCA	1800 H TCTGC : ::: M TTTGC	1870 H GGGGA ::::	H M GCTTG 1840	H CTCTG ::::: M CTCAG 1910

Fig. 70

2080 2100 2110 2120 2130 GACAGCGCCAGCCGAGGTGGTCCCCGCATCAGGTAATTCTGCCCAAGGCTCA :::::::::::::::::::::::::::::::::::	2140 AC-TGC	2180 2200 2200	2210 2220 2230 H AACCCACCATCA-TCCCAAACTCTCTGTCCTTT :::::::::::::::::::::::::::::	2240 2250 2260 2270 H GCCTTCATTCTCT-TACCCACCTCTACCTATGGGTCTC :: :: :: :: :: :: :: M GCACCCCTGAGGAGCAAGACTTTGTCAATGATCGATACCGGGAGTACCAGTGGATTGGGCTCAATGACAG 2260 2270 2280 2290 2310 2320
2080	H A(H AACCCAC	H GCCT
H GACAGCGCCZ	:		::::	:: ::
::::::::	M ATGGTGGGA(M TCCACACGAZ	M GCACCCTG/
M GACAGTGCCZ	2050		2190	2260

Fig. 7R

90 2320 2310 2320 CTTGTGG-GTATCTCAGCTCTCGCGT-CTT-TACCCTGTG-AT : .::: : :::::::::::::::::::::::::::::	2330 2340 H CCCAGCCCCGCCACTGACCATCTGTGA :: ::: ::: ::: ::: M CCTGACAGCTACTTCCTGTCTGGGAAACTGTGTGTCATGGTGTGGCATGACCAGGGACAGTGGAGTG 2400 2410 2420 2430 2440 2450	2370 2380 ccarrent 2380 ccarrent 2390 ccarrence creatercre creatercre creatercre carrence ccarrence ccarrence ccarrence ccarrence carrence	2420 2430 2440 2450 CCTCAGGCCTCTCCAAGGGTCCTCATCACCTATTGCA ::::::::::::::::::::::::::::::::::::	2470 2480 GCTCGGCCTATTTCCACTACTCC ::::::::::::::::::::::::
2280 2290 2290 2290	2330 H CCCAGCA(:: :: : : :: M CCTGACAGCTACTTCCTGTCTGGGGAGAA(2400 2400 2410	2360 2370 HCCCTTCC-CTGCCATTGGGCCCT :::::::::::::::::::::::::::::::::	2410 2420 H GCCAGCCCCACAGAGCATCCTCAG- ::::::::::::::::::::::::::::::::::::	2460 HGCCTTCAGGGCTCGGC :::::::::::::: M ATGCCGAGACGGGCTGGCTCAGCGCAACCT

Fig. 7S

2490 2500 2530 CTTCA-TCCGCCTGTGTGCCGTCCCCTTTAGCTGC-CTCCTATTGATCTC ::::::::::::::::::::::::::::::::::	2540 AGGGA-AGCCTGGGAGTC-CC-TTCTCACCCCTC-AACCTCCGGAGT-CCAGGAGAAC :::::::::::::::::::::::::::::	590 2600 2610 2630 2630 2620 2620 2620 2620 2630 263	2650TTTGACTGTTTCATGGAAAACA	0 GGAAATAAATCTCTATTAAAC .:.::::::::::: AGGITTTACCCGGTAAGTCCCTAACTGCCTCTCATGTCAGCTGC 2980 3010 3020
2510 2520 CCTTTAGCTGC-CTCCT :::::::::: GGCCGTGCTCTGCGCTCCATGC 2710 2720 27	2570 CACCCCTC-AACCTC :::::::::::::::::::::::::::::::::	2620 TCT ::: AGTGCTCTTCCCCATG 2860 28	2650 TGGAAAACA- ::::::: GGTTTCTGGGAAACAC 2930	2670 AAATCTCTATTAA :::::::::: AAGTCCCTAAGTGCCTCAACTG 2990 3000 3C
2510 :GTCCCCTT: ::::::::	2550 TGGGAGTC-CC-TTCTC ::::::::::::::::::::::::::::	2610 AA-GCAACTACT :.:.:: CTCACATCAACTGCC/ 840 2850		2670 ATAAATCTC ::::::::::::::::::::::::::::::::
2490 2500 CTTCA-TCCGCCTGTGTGCC : :: : ::::::: CCTCAGATTTCCTGTGTACCCC 2680 27	0 .GCCTG .:: :: .GCTCTCGAGGCACAG 2760 27	2590 2600 2610 CCGTACCCCCA-CAGAGCCTTAA-GCAACTACT- ::::::::::::::::::::::::::::::::::::	2640 -TTTGACTGTTTCA : :::: :::: STGGGACTGAAATTCAGAG	2660 AGCCTTGGAAAT. :::: ::::: CTCACACGGCCTCAGGTTT
2490 H CTTCA-T : :: . M CCTCAGA 2680	2540 H AGGGA-AGC .::: ::: M GGGGACAGC 2750	2590 H CCGTACC ::: M TGCTGCC 2820	HTTT : M GGGGIGG 2890	H М СТСАСАС 2960

Fig. 7T

£		2690	, ()		6 1 6 7	2700
_	CGCT'1''''G'1''''	AAC	AC		CAAAA	CAAAAAAAAAAAAAA
		•	•••		•	
-	CCCTCGATN	TCGTNAGGGG	ACACTGTGCT?	TTCGATCTT	GATTGTCGAAG	CTCCTTGTCCCTCGATNTCGTNAGGGGACACTGTGCTATTCGATCTTGATTGTCGAAGAGTTTTAGGAT
	3040	3050	3060	3070	3080	3090
			2720		2730	
	H AAA	AAAAI	AAAAAAAAGGGCGGCC	DDE	25	
		•		••	•	
7 3	AGCAAAACC	AGGTGGAAAT/	M GGAGTACCAGCAAAACCAGGTGGAAATAAAGTTGTCTGAACCCCAAAGAAAAAAAA	BACCCAAAG	AAAAAAAAA	
3100	3110	3120	3130	3140	3150	

Fig. 7U